

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:53:30 ; Search time 8133.32 Seconds  
(without alignments)  
11558.757 Million cell updates/sec

Title: US-10-735-098-3  
Perfect score: 2169  
Sequence: 1 atgtgtaaacgaattatgg.....tcaggagggtggaataatga 2169

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
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- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	100.0	2169	2169	1	AF123382	AF123382 Neisseria
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3	100.0	2169	2169	6	BD074756	BD074756 Neisseria
4	1562.4	72.0	2124	1	AF123383	AF123383 Neisseria
5	1562.4	72.0	2124	6	A98976	A98976 Sequence 9
6	1562.4	72.0	2124	6	BD074759	BD074759 Neisseria
7	1454.2	67.0	326301	1	NMA622491	AL162257 Neisseria
8	1453.6	67.0	2519	1	AF072890	AF072890 Neisseria
9	1375.8	63.4	2226	1	AF123380	AF123380 Neisseria
10	1375.8	63.4	2226	6	A98972	A98972 Sequence 5
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14	1304.8	60.2	2277	1	AF022781	AF022781 Neisseria
15	1304.8	60.2	2277	6	A98968	A98968 Sequence 1
16	1304.8	60.2	2277	6	BD074755	BD074755 Neisseria
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18	1301.6	60.0	2537	1	AF031432	AF031432 Neisseria
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23	439.2	20.2	1000	6	AX374691	AX374691 Sequence
24	222.4	10.3	3398	1	NMLBPAG	X79838 N.meningiti
25	105.2	4.9	3720	14	S76368	S76368 ORF 5' of E
26	105.2	4.9	43658	14	HSV3PRGEN	M86409 Herpesvirus
27	105.2	4.9	112930	14	HSGEND	X64346 Salmirine
28	105.2	4.9	214836	10	AC007305	AC007305 Mus muscu
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30	105	4.8	251960	2	AC107279	AC107279 Rattus no
31	104.6	4.8	194060	2	AC125897	AC125897 Rattus no
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33	103.8	4.8	271336	2	AC111017	AC111017 Mus muscu
34	103.6	4.8	244595	2	AC095144	AC095144 Rattus no
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38	103.4	4.8	227411	10	AC130821	AC130821 Mus muscu
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# ALIGNMENTS

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ACCESSION	AF123382.1	GI:4884690				
VERSION						
KEYWORDS						
SOURCE	Neisseria meningitidis					
ORGANISM	Neisseria meningitidis					
REFERENCE	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;					
AUTHORS	Neisseriaceae; Neisseria.					
	1 (bases 1 to 2169)					
	Petterson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and					
	Tomassen,J.					

TITLE  
Sequence variability of the meningococcal lactoferrin-binding  
protein lbpB  
JOURNAL  
Gene 231 (1-2), 105-110 (1999)  
MEDLINE  
99250255  
PUBMED  
10231574  
REFERENCE  
2 (bases 1 to 1169)  
AUTHORS  
Petersson, A., van der Biezen, J., Jørgensen, V., Hendriksen, J., and  
Tomassen, J.  
TITLE  
Direct Submision  
JOURNAL  
Submitted (26-JAN-1999) Department of Molecular Cell Biology,  
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands  
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Query Match 100.0%; Score 2169; DB 1; Length 2169;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 2169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GGGGGCAATTTGGCGTGAGCTTGTTCGAATCAACGGCGACCGGTACCCCGTCACT 120

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ACCESSION A98970  
VERSION A98970.1 GI:6781930  
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ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
1 (bases 1 to 2169)  
Petersson-Fernholm, A.M. and Tommassen, J.P.  
TITLE NEISSERIA LACTOFERRIN BINDING PROTEIN  
JOURNAL Patent: WO 9909176-A 3 25-FEB-1999;  
UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNKA MAR (NL)  
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ORIGIN

Query Match 100.0%; Score 2169; DB 6; Length 2169;  
Best Local Similarity 100.0%; Pred. No. 0;  
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RESULT 3

BD074756

LOCUS

BD074756

DEFINITION

Neisseria lactoferrin-binding protein.

ACCESSION

BD074756

VERSION

BD074756.1

GI:22620359

KEYWORDS

JP 2001514894-A/2.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 2169)

AUTHORS

Felnholm, A.M.P. and Thomassen, J.P.M.

TITLE

Neisseria lactoferrin-binding protein

JOURNAL

Patent: JP 2001514894-A 2 18-SEP-2001.

COMMENT

UNIVERSITY OF UTRECHT, TECHNOLOGY FOUNDATION

OS

Unidentified

PN

JP 2001514894-A/2

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GB

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PI

ANICA MARGARETA PETERSON FELNHOLM, JOHANNES PETRUS MARIA

THOMASSEN

PC

C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22, C07K16/12,

PC

C12N1/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC

C12N15/00

CC

Strandedness: Double;

CC

Topology: Linear;

CC

Neisseria lactoferrin-binding protein

PH

Key

Location/Qualifiers

FT

source

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FEATURES

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Query Match

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2169;

DB

6;

Length

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100.0%;

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Qy

1

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60

Db

1

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LOCUS  
DEFINITION Neisseria meningitidis strain 881607 lactoferrin-binding protein precursor (lbpB) gene, complete cds.  
ACCESSION AF123383  
VERSION AF123383.1 GI:4884692  
KEYWORDS  
SOURCE  
ORGANISM Neisseria meningitidis  
Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
REFERENCE 1 (bases 1 to 2124)  
AUTHORS Petersson, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tomassen, J.  
TITLE Sequence variability of the Meningococcal lactoferrin-binding protein lbpB  
JOURNAL Gene 231 (1-2), 105-110 (1999)  
MEDLINE 99250255  
PubMed 10231574  
REFERENCE 2 (bases 1 to 2124)  
AUTHORS Petersson, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tomassen, J.  
TITLE Direct Submission  
JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands  
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QY 1798 GGCACTACGTCATTTCAAAAGGATAGCTATCGGAATCAAGCGGCGGAAAGGAGGAGG 1857  
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QY 1858 GTTGATTTTGTGCGAAGTCTCTTTCAGTGAAGTTCAGAGAAAGGAGGAGGAGGAGG 1917  
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QY 1918 GCTTTTATATTTGAAAAAGGTTGATTCGATCGCAACGGTTTCCACGCTTTCGCGCTACT 1977  
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QY 1978 CGTGAAAAATGTTGTTGATTTCTCTGGCAAGGTTTCGACTAATCCCAAGTTTAAAGCC 2037  
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QY 2038 AGTAACTCTCTGTAAGAGGAGGATTTTATGTCGCGAGGCGGAGAGGTTGGTGGTAA 2097  
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QY 2098 ATTATCGACAGTACCGGAAATCGGCTGTTGTTTCGTCGGAAGAAAGATATGAGGAG 2157  
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RESULT 6

BD074759

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD074759 2124 bp DNA linear PAT 27-AUG-2002  
Neisseria lactoferrin-binding protein.

BD074759 1 GT:22620362

JP 2001514894-A/5.

unidentified

unclassified.

1 (bases 1 to 2124)

Felholm, A.M.P. and Thomsen, J.P.M.

Neisseria lactoferrin-binding protein

Patent: JP 2001514894-A 5 18-SEP-2001;

UNIVERSITY OF UTRICHT, TECHNOLOGY FOUNDATION

OS Unidentified

PN 2001514894-A/5

PD 18-SEP-2001

PF 10-AUG-1998 JP 2000509840

PR 15-AUG-1997 GB 9717423.9, 05-FEB-1998 GB 9802544.8 PI

ANICA MARGARETA PETERSON FELNHOLM, JOHANNES PETRUS MARIA PI

THOMSEN

PC C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22,

PC C07K16/12,

PC C12N1/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC

C12N15/00

CC Strandedness: Double;

CC Topology: Linear;

CC Neisseria lactoferrin-binding protein

FF Key Location/Qualifiers

FT source 1..2124

FT Location/Qualifiers

approved

source

1..2124

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ORIGIN

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Matches 1835; Conservative 0; Mismatches 286; Indels 51; Gaps 5;

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QY 61 GCGCGCAATTCGGCGTCAGCGCTGTTGTCGAATCAACGCCGACCGCGTACCCCGTCACT 120
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QY 121 TTCAAGTCTAAGGACGTTCCCACTTCGGCCCTGCGGGTCTTTCGGTAGAAGCAACCGCG 180
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QY 181 GTCAACGACCGCGCTGCTGGGCAATGCGGCTGTTGAGACGGAATATGCACTTCT 240
DB 181 GTCAACGACCGCGCTGCTGGGCAATGCGGCTGTTGAGACGGAATATGCACTTCT 240

QY 241 CGTGAAGATGACCGGCAATTCGCGATAGCAAAACGACGAGAAAGAGTCTGTTTAAA 300
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QY 361 GAAATTCATAACGTAATCTGAGGCAAGCAATACCAATCGGAAATGAAATTAAGAAA 420
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DB 481 GAGTGGACTTCAAATACAGCACTACCAACCGGTTTGTATGACGTTTGTATAT 540

QY 541 TATCTCGGAGAACATCTTCCCAATCTTACCGAGCGCGGAAACGTTGAAATATTCGGC 600
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QY 718 AGGGATGCGGATGCGCGGAAACATCTGCGGAAATATACGGTTAAATTTTCGACAAAAA 777
DB 721 ACTGCCGACGACCGCGGAGGAAACATCTGCGGAAATATACGGTTAAATTTTCGACAAAA 780

QY 778 AACCTCGAAGTAAATTTGATTAATAATCAGTATGTCGAAAGAGAGATGATCTTAAAT 837
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QY 838 CCACTGACATTTACAACTTACCGCAACATTCGACGCAACCGCTTTTACCGGAGTGC 897
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QY 1018 CGGTTTATCAGTAACGACAAACAGCGTATTCGGCGTGTTCGCAAGGCAAAACAAAAACAG 1077
DB 1021 CGGTTTATCAGCAACGACAAACAGCGTATTCGGCGTGTTCGCAAGGCAAAACAAAAACAG 1080

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QY 1138 GATTCTCTAAATAATTTCCGTTGACGAGCGGACTGATGACCATGCGCGTAAGTTTCCATT 1197
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QY 1198 TCACATATGCCGATTTTGTTCATCCGACAAAATTTCTTGTGCAAGGCGGTGAATTTCT 1257
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QY 1498 ACCGAGAGAGAACTGATGAGAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1557
DB 1482 --CGAAGTCTGAGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1533

QY 1558 GAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGGAGG 1617
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QY 1678 CTTTCTCTGAAAGGATTCGCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1737
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QY 1738 TATACCGGACTTTGGAAGCGGCTATTCGGGTCGCGGATGAGAGGAGGAGGAGGAGGAGGAG 1797
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QY 1858 GTTGATTTTGGTGGCGAAGTCCGCTTTCAGGTAAGTTTGCAGAGAAAATGATACACACCC 1917
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QY 1918 GCTTTTATTTGAAAAGGAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1977
DB 1873 GCTTTTATTTGAAAAGGAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1932

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Db	2053	ATTATCCACAGCGACCGGAAATTCGGTGGTATTTGGCGGCGAAGAAAGATGACAGGAG	2112	
QY	2158	GTGGAAAAATGA	2169	
Db	2113	GCAACAGATGA	2124	
RESULT 7				
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DEFINITION	Neisseria meningitidis serogroup A strain Z2491 complete genome;			
ACCESSION	segment 6/7.			
VERSION	AL162757 AL157959			
KEYWORDS	AL162757.2 GI:7380371			
SOURCE	Neisseria meningitidis Z2491			
ORGANISM	Neisseria meningitidis Z2491			
REFERENCE	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.			
AUTHORS	1 (bases 1 to 326301)			
	Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C., Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T., Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N., Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K., Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M., Skelton,J., Whitehead,S., Spratt,B.G. and Barrall,B.G.			
TITLE	Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491			
JOURNAL	Nature 404 (6777), 502-506 (2000)			
MEDLINE	20222556			
PubMed	10761919			
REFERENCE	2 (bases 1 to 326301)			
AUTHORS	Parkhill,J.			
JOURNAL	Direct Submission			
	Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk			
COMMENT	Notes: Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web. URL, http://www.sanger.ac.uk/Projects/N_meningitidis/.			
FEATURES	Location/Qualifiers			
source	1..326301 /organism="Neisseria meningitidis Z2491" /mol_type="genomic DNA" /strain="Z2491" /db_xref="taxon:122587" /note="serogroup: A"			
repeat_unit	196..311 /note="REP 2; hmms hit to HMM REP 2 (1 - 109), score: 87.43"			
repeat_unit	434..453 /note=">= 90% match to ATTCNNNNNNNGGGAAT"			
repeat_unit	/label=DRS3 498..560 /note="Correia element; hmms hit to HMM Correia (1 - 62), score: 78.71" /label=Correia 562..604 /note="Correia element; hmms hit to HMM Correia (114 - 156), score: 51.92"			
repeat_unit	/label=Correia complement(667..676) /note="Core DNA uptake sequence: gccgtctgaa"			
misc_feature	/label=DUS complement(668..1813) /gene="dapE"			
gene				

CDS				
	complement(668..1813)			
	/gene="dapE"			
	/EC number="3.5.1.18"			
	/note="NMA1730, dape, succinyl-diaminopimelate desuccinylase, len: 381aa; similar to many eg. SW:P24176 (DAPE_ECOLI) dape, succinyl-diaminopimelate desuccinylase from Escherichia coli (375 aa) fasta scores; E(): 0, 56.9% identity in 371 aa overlap. Contains Pfam match to entry PF01546 Peptidase_M20."			
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fasta scores; E(): 0, 96.7% identity in 183 aa overlap.
Contains Pfam match to entry PF00127 copper-bind, Copper
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(901 aa) fasta scores; E(): 0, 58.0% identity in 920 aa
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Prosite match to PS01312 Protein secA signatures."
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67.0%; Score 1454.2; DB 1; Length 326301;
Best Local Similarity 81.9%; Pred. No. 1.5e-290;
Matches 1742; Conservative 0; Mismatches 343; Indels 42; Gaps 4;

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Db	18921	GGCGCAATTTTCGGCGTGAGCCTGTGTGCGAATCAACGCCGCGGTACCCCGTCAC	18862
QY	121	TTCAAGTCTAAGGACGTTTCCCATCTTCGCCCTTCGCCGCTTCGTTAGAAACACGCGC	180
Db	18861	TTCAAGTCTAAGGACGTTTCCCATCTTCGCCCTTCGCCGCTTCGTTAGAAACACGCGC	18802
QY	181	GTCAACGACCGCCCGTTCGGTTCGGCAATGCGGCTCTTCAGACGGGATATCTGTTTTCAT	240
Db	18801	GTCAACGACCGCCCGTTCGGTTCGGCAATGCGGCTCTTCAGACGGGATATCTGTTTTCAT	18742
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Db	18741	CGTGAAGATGGCAGCGCAATCCCGATAGCAACAAAGCAAGAGAAAGCTGTCGTTTAA	18682
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Db	18621	GAATTTCAATAACGCAATCTTAATGTAGAAATTAGGACATCAGAAATGAAATATAAATA	18562
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QY	541	TATCTCGGAGAACATCTTCCCAATCTTACCGGCGCGGCAACGGTGAATATTTCCGGC	600
Db	18441	TATTCGGGAGAACATCTTCCCAATCTTACCGGCGCGGCAACGGTGAATATTTCCGGC	18382
QY	601	AACCTGCAATATATGACCGGATGCCATAGCTCATCGAGAGGTAA--GGGGTTTCCAGT	657
Db	18381	AACCTGCAATATATGACCGGATGCCATAGCTCATCGAGAGGTAA--GGGGTTTCCAGT	18322
QY	658	GTGGATTTGGTTATACCATATATGTTAATGTAATGGAATTTGGGCGAGCTTCTTATGAGCT	717
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QY	718	AGGGATGCCCATGCGCGGGAACATCTCTCGCGAATATACGGTTAAATTTTCGACAAAAA	777
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Db	18081	AAAGTTAACACCGAGTGAAGACGCAACACGCTGATAAGAAATATTTGTTTCCATACC	18022
QY	958	GATGCGGATCAGCGCTTGAGGCGGCTTTTTCGGCGATAACCGAGAGAGCTTGCCTGG	1017
Db	18021	GATGCGGATCAGCGCTTGAGGCGGCTTTTTCGGCGATAACCGAGAGAGCTTGCCTGG	17962
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QY	1198	TCCACTATGCCCGATTTTGGTTCATCCCGACAAATCTTCTGTCGAAGCGGCTGAAATTCCT	1257
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Db	17721	TTGCTTAGCCAGATCTCAACCATCGATCTTCCCGACGCGAGAAATGACCATCCGTC	17662
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QY	1672	ATCGACCTTTCTGAAAGGTTTCCGACCGCGGAGCGACATTCGCAAAATTTGAA	1731
Db	17301	ATCGACCTTTCTGAAAGGTTTCCGACCGCGGAGCGACATTCGCAAAATTTGAA	17242
QY	1732	GCACGCTATACCGGCACTTGGGAGCGGCTATCGGCGTCCGATGAAGAGCGGACAG	1791
Db	17241	GCACGCTATACCGGCACTTGGGAGCGGCTATCGGCGTCCGATGAAGAGCGGACAG	17182
QY	1792	CTAGATGGCACTAGCTCCATTCAGAGGATAGCTATCGCAATCAAGCGCAAGAGAGAA	1851
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QY	1852	TTTGAGCTTGAATTTGGTGCGAAGTCCGTTTCAAGTGAAGTTGACAGAAAAATGATA	1911
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QY	1912	CACCCCGCTTTTATATTGAAGAGGTTGATGAGGCAACCGTTTCCAGCTTTGGCG	1971
Db	17094	GAAGCTGCTTTCTATATTGAAGAGGTTGATGATGAGGCAACCGTTTCCAGCTTT	17035
QY	1972	CGTACTCGTGAATGTTGTTGATTTGCTGGGCAAGTTTCAATATCCCAAGTTT	2031
Db	17034	CGCACTCGGATGAACGCACTCAATTTCTGGGAAATGTTTCGACCAACCCCAACCTTC	16975
QY	2032	AAAGCCAGTATCTTCTGATAGAGAGAGATTTTATGTTCCGAGCGGAGAGATTCGGT	2091
Db	16974	CAAGCTAGTATCTTCTGATAGAGAGAGATTTTATGTTCCGAGCGGAGAGATTCGGT	16915
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RESULT 8

AF072890

LOCUS

DEFINITION

Neisseria gonorrhoeae lactoferrin binding protein B precursor (lbpB) gene, complete cds.

ACCESSION

AF072890

VERSION

AF072890.1

GI:4106392

KEYWORDS

SOURCE

Neisseria gonorrhoeae

ORGANISM

Neisseria gonorrhoeae

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 2519)

Biswas, G.D., Anderson, J.E., Chen, C.J., Cornelissen, C.N. and Sparling, P.F.

IDENTIFICATION and functional characterization of the Neisseria gonorrhoeae lbpB gene product

Infect. Immun. 67 (1), 455/459 (1999)

JOURNAL

MEDLINE

PUBMED

99081783

9864256

REFERENCE

2 (bases 1 to 2519)

Biswas, G.D., Anderson, J.E., Cornelissen, C.N. and Sparling, P.F.

Direct Submission

Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521

Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA

FEATURES

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Location/Qualifiers

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/mol\_type="genomic DNA"

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364..2484

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/product="lactoferrin binding protein B"

1902..1911

/gene="lbpB"

/note="encodes gonococcal uptake sequence"

ORIGIN

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Db	367		
QY	121	TTCAAGTCTAAGAGCGTTCCCACTT---CGCCCCCTCGCGGCTCTTCGGTAGAACCACG	177
Db	427		
QY	178	COGCTCAACAGCCGCGCGTTCGGTGGGCAATGCGGCTGTTCAGACGGAATACTGCTTTT	237
Db	487		
QY	238	CATCGTGAAGATGGCACGGCAATTCGCCATAGCAACCAAGACAGAGAAAGCTGCGTTT	297
Db	547		
QY	298	AAAGAAGTGATGTTCTGTTTTTATACGGTTTCAAAAGAAAAATAAACTTCAACAATTTAA	357
Db	607		
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Db	847		
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QY	778	AACTGGAAGGTAAAGTTGATTTAAAAATCAGTGTGCAAAAGACAGATGATCCTTAAAT	837
Db	1087		
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Db	1147		
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Db	1207		
QY	958	GATGCCGATCAGCGGCTTGAGGGCGGTTTTTTTCGGCGATACCGGAGAGAGCTTGCGGG	1017
Db	1267		
QY	1018	CGGTTTATCAGTAAACGACAAACAGCGTATTTCGGCGTGTTCGACGCAACAAAAACAGAG	1077

Db	2335	ACTATTTTCAATGAAGTGGGAAA	2359
Db	AF123380	2226 bp	DNA
LOCUS	Neisseria meningitidis strain H44/76	linear	BCT 24-MAY-1999
DEFINITION	precursor (lbpB) gene, complete cds.		
ACCESSION	AF123380		
VERSION	AF123380.1	GI:4884686	
KEYWORDS	Neisseria meningitidis		
SOURCE	Neisseria meningitidis		
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
REFERENCE	Pettersson, A., van der Biezen, J., Joosten, V., Hendriksen, J. and Tommassen, J.		
AUTHORS	Sequence variability of the meningococcal lactoferrin-binding protein lbpB		
TITLE	Gene 231 (1-2), 105-110 (1999)		
JOURNAL	99250255		
MEDLINE	10231574		
PUBMED	2 (bases 1 to 2226)		
REFERENCE	Pettersson, A., van der Biezen, J., Joosten, V., Hendriksen, J. and Tommassen, J.		
AUTHORS	Direct Submission		
TITLE	Submitted (26-JAN-1999) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands		
JOURNAL	Location/Qualifiers		
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ORIGIN	Query Match 63.4%; Score 1375.8; DB 1; Length 2226;		
	Best Local Similarity 80.4%; Pred. No. 2e-274;		
	Matches 1710; Conservative 0; Mismatches 357; Indels 60; Gaps 6;		
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## RESULT 10

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DEFINITION Sequence 5 from Patent WO9909176.
ACCESSION A98972
VERSION A98972.1 GI:6781932
KEYWORDS
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Patent: WO 9909176-A 5 25-FEB-1999;  
UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIKA MAR (NL)

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## ORIGIN

Query Match 63.4%; Score 1375.8; DB 6; Length 2226;  
Best Local Similarity 80.4%; Pred. No. 2e-274;  
Matches 1710; Conservative 0; Mismatches 357; Indels 60; Gaps 6;  
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2050 GGTACTATTTCAATAATGATGGGAA 2076

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BD074757

LOCUS BD074757 2226 bp DNA linear PAT 27-AUG-2002  
DEFINITION Neisseria lactoferrin-binding protein.  
ACCESSION BD074757  
VERSION BD074757.1 GI:22620360  
KEYWORDS JP 2001514894-A/3.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2226)  
AUTHORS Feinholm, A.M.P. and Thomassen, J.P.M.  
TITLE Neisseria lactoferrin-binding protein  
JOURNAL Patent: JP 2001514894-A 3 18-SEP-2001;  
UNIVERSITY OF UPECHT, TECHNOLOGY FOUNDATION  
COMMENT OS Unidentified  
PN JP 2001514894-A/3  
PD 18-SEP-2001  
PF 10-AUG-1998 JP 2000509840  
PR 15-AUG-1997 GB 9717423.9 05-FEB-1998 GB 9802544.8 PI  
ANICA MARGARETA PETERSON FEINHOLM, JOHANNES PETRUS MARIA PI  
THOMASSEN  
PC C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22,  
C07K16/12,  
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Strandedness: Double;  
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FH Key Location/Qualifiers  
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FEATURES  
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1..2226  
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# RESULT 12

AE002504/c

LOCUS

DEFINITION

Neisseria meningitidis serogroup B strain MC58 section 146 of 206

of the complete genome.

ACCESSION

AE002504 AE002098

VERSION

AE002504.1 GI:7226785

KEYWORDS

SOURCE

Neisseria meningitidis MC58

ORGANISM

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria.

REFERENCE

AU

1 (bases 1 to 9955)

Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,

Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,

Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,

Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,

Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,

Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,

Pizza, M., Grandi, G., Sun, L., Scarlato, V., Massignani, V.,

Rappuoli, R. and Venter, J.C.

Complete genome sequence of Neisseria meningitidis serogroup B

strain MC58

Science 287 (5459), 1809-1815 (2000)

20175755

10710307

2 (bases 1 to 9955)

Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,

Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,

Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,

Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,

Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,

Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,

Pizza, M., Grandi, G., Sun, L., Scarlato, V., Massignani, V.,

Rappuoli, R. and Venter, J.C.

Direct Submission

Submitted (17-MAR-2000) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

FEATURES

Location/Qualifiers

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identified by sequence similarity; putative"

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gene		5292	GTATATTATTCCGGAGAAACGTCTTCCCAATCTTTTACCGAGCGCGGGAACGGTGCAATAT	5233
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gene		5232	TCCGGTAACTGGCAATATATGACCGATGCCAATCGTCATCGGACAGTAAAGCGGTTTTCC	5173
CDS		655	AGTGTGGATTGGGTTATTACCAATATTATGTTAAATTTGGGACAGCTTCTTATGAG	714
gene		5172	AGTACGGATTGGGTTTATACCAATATTATGTTAAATTTGGGCAACTTCTTATGAG	5113
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gene		4992	GAGCCCCAAAAAAGCGCTGACCAATTTACGACATTTACGCAACATTTGGAAGCGCAACCGCTTT	4933
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gene		4932	ACCGGAGTGCCAAAGTTAGCACCGAGGTGAAGACGACACACGCTGATATAAGCAATATTG	4873
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gene		4872	TTTTTCCATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCGATAAACGGAGAA	4813
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gene		4692	ACCAAAATCTTGGATTCTCTAAAAATTTCCGTTGACGAGGGGACATGATGACCATCCCGGT	4633
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LOCUS	AX044033	349980 bp	DNA linear PAT 24-NOV-2000
DEFINITION	Sequence 112 from Patent WO0066791.		
ACCESSION	AX044033		
VERSION	AX044033.1 GI:11342917		
KEYWORDS			
SOURCE	Neisseria meningitidis		
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
REFERENCE	1		
AUTHORS	Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C., Masignani, V., Galeotti, C., Moxa, M., Ratti, G., Scariselli, M., Scariato, V., Rappuoli, R., Frazer, C. M. and Grandi, G.		
TITLE	Neisseria genomic sequences and methods of their use		
JOURNAL	Patent: WO 0066791-A 112 09-NOV-2000;		
FEATURES	CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)		
	Location/Qualifiers		

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Best Local Similarity	79.0%	Pred. No. 3.4e-271;	
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Qy	775	AAAAACCTGGAAGGTAAGTTGATTAATAATCAGTATGTGCAAAAGA-----GAGAT	825
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ORIGIN

Query Match		60.2%; Score 1304.8; DB 1; Length 2277;
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QY	121	TTCAAGTCTAAGGAGTTCCTACTTCGCCCTCGCGGTCTTCGGTAGAACCACGCG 180
Db	220	TTCAAGTCTAAGGAGTTCCTACTTCGCCCTCGCGGTCTTCATAGAAATCACGCG 279
QY	181	GTCAACACGCCGCGTGGCGCAATGCGCTGTGTGAGACGGAATCTGCTTTTCAT 240
Db	280	GTCAACCGCGCGCGTGGCGCAATGCGCTGTGTGAGACGGAATCTGCTTTTCAT 339
QY	241	CGTGAAGATGCGACGGCAATTTCCGATAGCAAAACAGCAGAGAAAAGCTGTGCTTAAA 300
Db	340	CGTGAAGATGCGACGGAAATTTCCAAATAGCAAAACAGCAGAGAAAAGCTGTGCTTCAA 399
QY	301	GAGGTGATGCTCTGTTTTATACGTTTCAAGAAATAAATCTTCAACAATTTAAAGC 360
Db	400	GAGGTGATGCTCTGTTTTATACGTTTCAAGAAATAAATCTTCAACAATTTAAAGC 459
QY	361	GAAATTTCAAAACGTAATCTTGGAGCAAGCATTACCATCGGAAATGAAATTAATAA 420
Db	460	GAAATTTCAAAACGTAATCTTGGAGTGAATAATAGGACATCAGAAAGGAAATTAATAA 519
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QY	481	GAGAAACATCGGATGAAGACGTTTCTAATCGTTTAGCTATGACGTTTCTATAT 540
Db	577	AAGTGAATTTAGATGACGTTTCTAATCGGTTTCTAATCGGTTTCTATAT 636
QY	541	TATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGAAACGTTGAAATATTCGGC 600
Db	637	TATTCGGAGAACGTTCTTCCCAATCTTTACCGAGTGGGAAACGTTGAAATATTCGGT 696
QY	601	AACGCGCAATATGACCGATGCCATAGCTCATCGAGAGGTAAAGGGGTTTCCAGTG 660
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QY	661	GAATTTGGTTATACCATATATATGTAATGAAATTTGGGACGCTTCTTATGAGGCTAG 720
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QY	781	CTGGAAGGTAAAGTTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCCTTAAATCCA 840
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QY	841	CTGACCATTTTACAACATACCGCAACATTTGGACGGCAACCGCTTTTACCGGCGAGTGCCAAA 900
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QY	1441	ATTTCCGAGATGATTAACGCGAAGATGAAGTCCAGGAGAGAGAGAGAGAGAGAGAG 1500
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QY	1501	GAAGAGAACTGTATGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db	1564	GACGAAGCCACAGAAAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1596
QY	1561	ACTGAAGAAACTGAAGAAACTGAAGAAACTGAAGAAACTGAAGAAACTGAAGAAACTGA 1620
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QY	1621	GCGGTTCCAGGAGATCTCTGCGCACTCGGAGAGCTCTAAAGCGAGGAGACATCGACCT 1680
Db	1642	GCGAGTTCAAAACGCGCATCTGCTGCTGCGGAGAGCTCTAAAGCGAGGAGATCGACCT 1701
QY	1681	TTCTGTAAGGTATCCGACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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QY	1741	ACCGGCACTTGGGAAGCGGATTCGGCTGCGGAGATAAGAAAGGAGAGAGAGAGAGAG 1800
Db	1762	ACCGGCACTTGGGAAGCGGATTCGGCAAAACCAATTCATGGAACAATCATCGGAT--- 1818
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Db	1819	-----AAAGAGCGGCAAAAGAGAGATTTTACCGTT 1848
QY	1861	GATTTTGTGGAAGTTCGCTTTTACGTTAAGTTGACAGAAAAAATGATACACACCCCGCT 1920
Db	1849	GATTTTGTGGAAGTTCGATTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1908
QY	1921	TTTTATTTGAAAAAGGTGATGATGCAACGGTTTCCAGCTTTGCGGCGGATCTCGT 1980
Db	1909	TTCCGTATTTGAAAAAGGTGATGATGCAACGGTTTCCAGCTTTGCGGCGGATCTCGG 1968
QY	1981	GAAATGTTGTTGATTTGCTCTGCGCAAGCTTCGACTTAATCCCAAGTTTAAAGCGAGT 2040



Db 1969 GATGACGGCATGACCTTTCCGGCGAGGGTTTCGACCAAAACCGCAGATCTTCAAGCTAAT 2028  
QY 2041 AATCTTCTGTAGAGGAGGATTTATGTGTCGCGAGCGGCGCAGAGTTGGTGTGTAATATT 2100  
Db 2029 GATCTTCTGTAGAGGAGGATTTATGTGTCGCGAGCGGCGGAGGAGGATTTGGCGGTATTATT 2088  
QY 2101 ATCGACAGTGCACCGGAAA 2118  
Db 2089 TTCAATAATGATGGGAAA 2106

RESULT 15  
A98968  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

A98968  
Sequence 1 from Patent WO9909176.  
A98968  
A98968.1 GI:6781928  
Neisseria meningitidis  
Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
1 (bases 1 to 2277)  
Pettersson-Fernholm A.M. and Tommassen, J.P.  
NEISSERIA LACTOFERRIN BINDING PROTEIN  
Patent: WO 9909176-A 1 25-FEB-1999;  
UNIV UTRECHT (NL); PETTERSSON FERNHOLM ANNIKA MAR (NL)  
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DLSYKQFNSRLGDFVYVYSGRPSLPSACTVEYSGWQYMDAKRHRAKAVGI  
DNLGYTFYGNVDGATSVAAKDVDEREKHPAKYTFDGNKLTLSHELLKNQIVKPSKQ  
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Query Match 60.2%; Score 1304.8; DB 6; Length 2277;  
Best Local Similarity 79.1%; Pred. No. 1e-259;  
Matches 1675; Conservative 0; Mismatches 332; Indels 111; Gaps 6;

QY 1 ATGTGTAACCGAATTATGGCGCATTTGCTTGTGTGCCCTTACCTTTTGGCATCTTGATC 60  
Db 100 ATGTGTAACCGAATTATGGCGCATTTGCTTGTGTGCCCTTACCTTTTGGCATCTTGATC 159  
QY 61 GCGGCAATTCGCGGTGCAGCTTGTGTGAATCAACGCGGACCGGTACCCCGTCACT 120  
Db 160 GCGGCAATTCGCGGTGCAGCTTGTGTGAATCAACGCGGACCGGTACCCCGTCACT 219  
QY 121 TTCAAGTCTAAGACGTTCCACATTCGCCCTCCCGGTCTTCGGTAGAACAACGCCCG 180  
Db 220 TTCAAGTCTAAGACGTTCCACATTCGCCCTCCCGGTCTTCGGTAGAACAACGCCCG 279  
QY 181 GTCAACGACCCCGGTTCGGTGGCGCAATGGGCTGTTGAGACGGAATACCTGCTTTTCAT 240

Qy	1321	TGCGATTTTCTGACTATGTCGAACTCGGACGGATATAAAACCGACCGCCCGCCGTCAAA	1380
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Qy	1381	CCGAGGCGCAGGATGAGAGGATTCGACATTCGATATGCGAAGAAAGCGAAGACGAA	1440
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Db	1504	ATCGCGGATGAGAGAGGACCGAGATGACGCGCGAGAGATGAAGGCGAGCGAAGAA	1563
Qy	1501	GAAGAAGAACTGTATGAAGACGAGAGGAGAAACCCGGAAGAACTGAAGAACTGAAGAA	1560
Db	1564	GACGAAGCCACAGAAACGGAAGACGCGCGAAGAA-----	1596
Qy	1561	ACTGAAGAACTGAGAAACTGAAGAACTGAAGAAATCCCGACAGAGAAAGGCAAC	1620
Db	1597	-----GACGAAGCTGAAGAACTGAGAAAGATTCGTCG---GCAGAGGCAAC	1641
Qy	1621	GCGGTTTCAGGCGATCCTGCCACTCCGGAAGCTCTAAAGGAGGAGACATCGACCTT	1680
Db	1642	GCGAGTTCAAACGCCATCCTGCTCTCCGGAAGCTCTAAAGGAGGAGATTCGACCTT	1701
Qy	1681	TTCTGTAAAGGTATCCGACGCGGAGAGCCGACATTCGCAATTTGGRAAGACGCTAT	1740
Db	1702	TTCTGTAAAGGTATCCGACGCGGAGAAACGAATATTCGCAAACTGGAGAGACGCTAT	1761
Qy	1741	ACCGCACCTTGGGAAGCGGTATCGCGTGCAGATAGAAAGGCGAACAGCTAGATGCG	1800
Db	1762	ACCGCACCTTGGGAAGCGGTATCGGCAACCCATTCATGGGACAAATCATCGCGAT---	1818
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Qy	1861	GATTTTGGTGGAGTCGCTTTTCAGTAACTTGACAGAAATAATGATACACACCGCT	1920
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Qy	1981	GAAAATGCGTGTGATTTGCTGGGCAAGGTTGCACTAATCCCAAGTTTAAAGCCAGT	2040
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Qy	2041	AATCTTCTGTAGAGGAGGATTTTATGTTCCGCGAGCGGAGTTGGGTGCTAATATT	2100
Db	2029	GATCTTCTGTAGAGGAGGATTTTACGGCCCGAAGCGGAGGAAATGGCGGTATTATT	2088
Qy	2101	ATCGACAGTGACCGGAAA	2118
Db	2089	TTCAATATGATGGGAAA	2106

Search completed: August 24, 2004, 23:47:12  
Job time : 8152.32 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:48:44 ; Search time 734.857 Seconds  
(without alignments)  
12538.967 Million cell updates/sec

Title: US-10-735-098-3  
Perfect score: 2169  
Sequence: 1 atgtgtaaaccgaattatgg.....tcgaggagggtgaaaaaatga 2169

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002s:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2169	100.0	2169	2	Aax23320 N. mening
2	1562.4	72.0	2124	2	Aax23323 N. mening
3	1454.2	67.0	2226	7	ACA41945 Prokaryot
4	1375.8	63.4	2226	2	Aax23321 N. mening
c 5	1360.8	62.7	110000	3	Continuation (2 of
c 6	1360.8	62.7	349980	3	Aaf21611 Neisseria
7	1304.8	60.2	2277	2	Aax23319 N. mening
8	1250.6	57.7	2262	2	Aax23322 N. mening
c 9	868.2	40.0	14652	3	AAa81482 N. mening
10	491.6	22.7	707	3	AAa81815 N. mening
11	439.2	20.2	1000	4	Aaf91389 N. mening
12	439.2	20.2	1000	6	ABK37769 DNA sequ
13	94.6	4.4	400	5	AAa81815 N. mening
14	94.6	4.4	963	5	AAa81815 N. mening
c 15	94	4.3	453	5	AAa81815 N. mening
16	94	4.3	708	5	AAa81815 N. mening
17	94	4.3	708	5	AAa81815 N. mening
18	92.8	4.3	1686	2	AAQ87587 DNA encod
19	92.8	4.3	2932	2	AAV15422 DNA encod
20	92	4.2	2334	5	AAa81815 N. mening
c 21	90.6	4.2	496	4	AAa81815 N. mening
c 22	90.6	4.2	496	4	AAa81815 N. mening
c 23	90.6	4.2	496	4	AAa81815 N. mening

c 24	90.6	4.2	496	4	ABA43847 Human bre
c 25	90.6	4.2	496	4	ABA24068 Probe #25
c 26	90.6	4.2	496	4	AAK28026 Human bon
c 27	90.6	4.2	496	4	AAK28026 Human bon
c 28	90.6	4.2	496	4	AAK02592 Human bra
c 29	90.6	4.2	496	4	ABS27626 Human liv
c 30	90.6	4.2	496	5	AAI02512 Probe #25
c 31	89.8	4.1	248	5	AAI02512 Human gen
c 32	89.8	4.1	305	4	AAI21797 DNA encod
c 33	89.8	4.1	305	4	AAI21797 Probe #11
c 34	89.8	4.1	305	4	ABA66871 Human foe
c 35	89.8	4.1	305	4	AAI47083 Probe #15
c 36	89.8	4.1	305	4	AAI47083 Human bre
c 37	89.8	4.1	305	4	ABA33942 Probe #12
c 38	89.8	4.1	305	4	AAK41027 Human bon
c 39	89.8	4.1	305	4	AAK15306 Human bra
c 40	89.8	4.1	305	4	ABS40624 Human liv
c 41	89.8	4.1	305	5	AAI07480 Probe #74
c 42	89.8	4.1	483	5	ABS15007 Human gen
c 43	89.6	4.1	276	4	AAI23164 Probe #13
c 44	89.6	4.1	276	4	ABA68266 Human foe
c 45	89.6	4.1	276	4	ABA35275 Probe #13

## ALIGNMENTS

RESULT 1  
AAX23320  
ID AAX23320 standard; cDNA; 2169 BP.  
XX  
AC AAX23320;  
XX  
DT 11-JUN-1999 (first entry)  
XX  
DE N. meningitidis strain M981 LbpB cDNA.  
XX  
KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;  
KW meningitis; diagnosis; treatment; ds.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2169  
FT /\*tag= a  
FT /product= "LbpB"  
XX  
PN WO9909176-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 10-AUG-1998; 98WO-EP005117.  
XX  
PR 15-AUG-1997; 97GB-00017423.  
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PR 05-FEB-1998; 98GB-00002544.  
XX  
(UYUT-) RIJKSUNIV UTRECHT.  
(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.  
XX  
Pettersson-Fernholm AM, Tommassen JPM;  
WPI; 1999-190165/16.  
P-FSDB; AAW93493.  
XX  
New lactoferrin-binding protein B polynucleotides - obtained from  
Neisseria meningitidis, used to develop products for the diagnosis,  
prevention and treatment of neisserial disease, e.g. meningitis.  
XX  
Claim 2; Page 82-86; 116pp; English.  
XX  
This invention describes novel lactoferrin-binding protein B (lbpB)  
strains of Neisseria meningitidis. The products of this invention can be  
used for vaccinating humans against neisserial disease e.g. meningitis.

*Handwritten signature*

CC	Antibodies raised against the proteins of the invention can be used for									
CC	diagnosing or treating neiserial disease in humans. The LbpB									
CC	polypeptides can also be used for identifying compounds which inhibit the									
CC	polypeptides									
XX										
SQ	Sequence	2169 BP;	675 A;	457 C;	550 G;	487 T;	0 U;	0 Other;		
	Query Match	100.0%;	Score	2169;	DB	2;	Length	2169;		
	Best Local Similarity	100.0%;	Pred. No.	0;						
	Matches	2169;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ATGTGTAACCGAATTATGCGGGCAATTCCTGTGTGTCCTTACTTTTGGCATCTTGCATC	60							
DB	1	ATGTGTAACCGAATTATGCGGGCAATTCCTGTGTGTCCTTACTTTTGGCATCTTGCATC	60							
QY	61	GGCGCAATTTTCGGCGTGCAGCGCTGTGTGCGAATCAAGCGCGACCGGTACCCCGTCACT	120							
DB	61	GGCGCAATTTTCGGCGTGCAGCGCTGTGTGCGAATCAAGCGCGACCGGTACCCCGTCACT	120							
QY	121	TTCAAGTCTAAGGAGCTTCCGACTTCGCGCCCTCGCGGCTCTCGGTAGAAACCAAGCGG	180							
DB	121	TTCAAGTCTAAGGAGCTTCCGACTTCGCGCCCTCGCGGCTCTCGGTAGAAACCAAGCGG	180							
QY	181	GTCAACCGACCGCGTGGTGGCAATGCGGCTGTGAGACGGAATACTGCTTTTCAAT	240							
DB	181	GTCAACCGACCGCGTGGTGGCAATGCGGCTGTGAGACGGAATACTGCTTTTCAAT	240							
QY	241	CCTGAAGTGGCAACCGCAATTCCTGATAGCAACCAAGCAAGAAAGCTGCTTTTAA	300							
DB	241	CCTGAAGTGGCAACCGCAATTCCTGATAGCAACCAAGCAAGAAAGCTGCTTTTAA	300							
QY	301	GAAAGTGATGTTCTGTTTTTATACGTTTCAAGAAATTAATCTTCAACACTTAAAGC	360							
DB	301	GAAAGTGATGTTCTGTTTTTATACGTTTCAAGAAATTAATCTTCAACACTTAAAGC	360							
QY	361	GAAATTCATACAGTAACTCTGAGGCAAGCAATTCACATCGGAAATGAAATTAATAA	420							
DB	361	GAAATTCATACAGTAACTCTGAGGCAAGCAATTCACATCGGAAATGAAATTAATAA	420							
QY	421	TATAATATCGGTTCTGTCAGTGCCTGTATGTGTTTACTAAACCGGAAAGATGAAAT	480							
DB	421	TATAATATCGGTTCTGTCAGTGCCTGTATGTGTTTACTAAACCGGAAAGATGAAAT	480							
QY	481	GAGAAACATCGGATGAAAGAGTCTTCTAATCGTTTAGGCTATGACCGTTTGTATAT	540							
DB	481	GAGAAACATCGGATGAAAGAGTCTTCTAATCGTTTAGGCTATGACCGTTTGTATAT	540							
QY	541	TATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGAACGGTGAATATTCGGC	600							
DB	541	TATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGAACGGTGAATATTCGGC	600							
QY	601	AACGGCAATATATGACCGATGCCATACGTCATCGGAGAGGTAAAGGGGTTTCCAGTGTG	660							
DB	601	AACGGCAATATATGACCGATGCCATACGTCATCGGAGAGGTAAAGGGGTTTCCAGTGTG	660							
QY	661	GATTTGGTTATACCATATATGTAATGTAATGAAATTTGGGCGAGCTTCTATGAGGCTAGG	720							
DB	661	GATTTGGTTATACCATATATGTAATGTAATGAAATTTGGGCGAGCTTCTATGAGGCTAGG	720							
QY	721	GATGCGGATGCGCGGAAACATCTCGCGAATATACGGTTAATTTTCGACAAAAA	780							
DB	721	GATGCGGATGCGCGGAAACATCTCGCGAATATACGGTTAATTTTCGACAAAAA	780							
QY	781	CTGGAAGGTAAAGTTGATTAATAATACGATATGTGCAAAAGAGAGATGATCTTAAATCCA	840							
DB	781	CTGGAAGGTAAAGTTGATTAATAATACGATATGTGCAAAAGAGAGATGATCTTAAATCCA	840							
QY	841	CTGACCAATTTACACATTAACGCAATTCGAGCGCAACCGCTTTTACCGCAGTGCCAAA	900							
DB	841	CTGACCAATTTACACATTAACGCAATTCGAGCGCAACCGCTTTTACCGCAGTGCCAAA	900							
QY	901	GTTAGCACCGAGGTGAAGACGCAACACGCTGATAAAGAAATATTTGTTTTTCCATACCGAT	960							

DB	901	GTTAGCACCGAGGTGAAGACGCAACACGCTGATAAAGAAATATTTGTTTTTCCATACCGAT	960
QY	961	CCCAGTACGCGCTTGAGGGCGGTTTTTTTCGCGGATACGAGAGAGCTTCCCGGGGG	1020
DB	961	CCCAGTACGCGCTTGAGGGCGGTTTTTTTCGCGGATACGAGAGAGCTTCCCGGGGG	1020
QY	1021	TTTATCAGTAAAGCAACAGCGGTATTTCCGCGTGTTCGAGGCAAAACAAAAACAGAGACA	1080
DB	1021	TTTATCAGTAAAGCAACAGCGGTATTTCCGCGTGTTCGAGGCAAAACAAAAACAGAGACA	1080
QY	1081	GCAACGCAATCAGATACAAATCTCTCCCTCGCGTCTGAAACACACCAAAATCTTGGAT	1140
DB	1081	GCAACGCAATCAGATACAAATCTCTCCCTCGCGTCTGAAACACACCAAAATCTTGGAT	1140
QY	1141	TCTCTAAAAATTTTCGGTTGACGAGGCGACTGATGACCAATTCGCGGTAAGTTTCCATTTCC	1200
DB	1141	TCTCTAAAAATTTTCGGTTGACGAGGCGACTGATGACCAATTCGCGGTAAGTTTCCATTTCC	1200
QY	1201	ACTATGCCGATTTTGGTTCATCCCGACAAATCTTCTTGTGGAAGGGCGTGAATTTCTTTTG	1260
DB	1201	ACTATGCCGATTTTGGTTCATCCCGACAAATCTTCTTGTGGAAGGGCGTGAATTTCTTTTG	1260
QY	1261	GTTAGCCAAAGAAAAACCAATCGAGCTTCCGACGAGGAAATGACCAATCTCGTCTTGT	1320
DB	1261	GTTAGCCAAAGAAAAACCAATCGAGCTTCCGACGAGGAAATGACCAATCTCGTCTTGT	1320
QY	1321	TGCGATTTTCTGACCTATGTGAACTCCGACGATGAAACCGACCGCCCGCTCAAA	1380
DB	1321	TGCGATTTTCTGACCTATGTGAACTCCGACGATGAAACCGACCGCCCGCTCAAA	1380
QY	1381	CCGAAAGGCGCAGATGAAGAGGATTCGGAACATTTGATTAATGCGGAAGAAAGCGAA	1440
DB	1381	CCGAAAGGCGCAGATGAAGAGGATTCGGAACATTTGATTAATGCGGAAGAAAGCGAA	1440
QY	1441	ATTTCCGAAGATGATAACGCGCAAGATGAAGTCAACGAAAGAGAGAACTGAAGAAAC	1500
DB	1441	ATTTCCGAAGATGATAACGCGCAAGATGAAGTCAACGAAAGAGAGAACTGAAGAAAC	1500
QY	1501	GAAAGAAATCTGATCAACGAGGAGGAAACCGGAAAGAACTCAAGAAATCTGAAGAA	1560
DB	1501	GAAAGAAATCTGATCAACGAGGAGGAAACCGGAAAGAACTCAAGAAATCTGAAGAA	1560
QY	1561	ACTGAAGAAATCTGAAGAACTGAAGAAATTCGCGACGAGAGAGGCAAC	1620
DB	1561	ACTGAAGAAATCTGAAGAACTGAAGAAATTCGCGACGAGAGAGGCAAC	1620
QY	1621	GGCGTTTACGAGGAGGATCTTCCGACCTCGGAAAGCTCTAAAGGCGAGGACATCGACCTT	1680
DB	1621	GGCGTTTACGAGGAGGATCTTCCGACCTCGGAAAGCTCTAAAGGCGAGGACATCGACCTT	1680
QY	1681	TTCTCTGAAGGATATCCGACGCGGAGCGGACATTCGCAATTTGGAAGAGCAGCGTAT	1740
DB	1681	TTCTCTGAAGGATATCCGACGCGGAGCGGACATTCGCAATTTGGAAGAGCAGCGTAT	1740
QY	1741	ACCGGCACTTTGGGAAGCGGTATTCGCGTTCGCGGATGAAGAAAGCGGCAACAGCTAGTGC	1800
DB	1741	ACCGGCACTTTGGGAAGCGGTATTCGCGTTCGCGGATGAAGAAAGCGGCAACAGCTAGTGC	1800
QY	1801	ACTACGTCATTTCAAAAGGATAGTATGCAATCAAGCGGCAAAACAGATTTTACGTT	1860
DB	1801	ACTACGTCATTTCAAAAGGATAGTATGCAATCAAGCGGCAAAACAGATTTTACGTT	1860
QY	1861	GATTTTGGTGGCAAGTTCGCTTTTTCAGGTAAAGTGAAGAAATGATACACACCCCGCT	1920
DB	1861	GATTTTGGTGGCAAGTTCGCTTTTTCAGGTAAAGTGAAGAAATGATACACACCCCGCT	1920
QY	1921	TTTTATATTAAGAAAGGTGTGATTTGCAACGTTTTTCCAGCTTTGGCGGCTACTCGT	1980
DB	1921	TTTTATATTAAGAAAGGTGTGATTTGCAACGTTTTTCCAGCTTTGGCGGCTACTCGT	1980
QY	1981	GAAATGGTGTGATTTGCTGGGCAAGGTTTCCGATTAATCCCAAAGTTTTTAAAGCCAGT	2040
DB	1981	GAAATGGTGTGATTTGCTGGGCAAGGTTTCCGATTAATCCCAAAGTTTTTAAAGCCAGT	2040

QY 2041 AATCTTCTGTAGAGGAGATTATATGTCGCGAGCGGCGAGAGTTGGGTGGTAATATT 2100  
DB |||||  
QY 2041 AATCTTCTGTAGAGGAGATTATATGTCGCGAGCGGCGAGAGTTGGGTGGTAATATT 2100  
DB |||||  
QY 2101 ATCGACAGTACCGGAAATCGCGTGGTATTTCGTCGGAAGAAAGATATGACGAGGTG 2160  
DB |||||  
QY 2101 ATCGACAGTACCGGAAATCGCGTGGTATTTCGTCGGAAGAAAGATATGACGAGGTG 2160  
DB |||||  
QY 2161 GAAATATGA 2169  
DB |||||  
QY 2161 GAAATATGA 2169  
DB |||||

RESULT 2  
AA232323  
ID AA232323 standard; cDNA; 2124 BP.

AC AAX232323;

DT 11-JUN-1999 (first entry)

XX N. meningitidis strain 881607 LbpB cDNA.

XX LbpB; lactoferrin binding protein; vaccine; neisserial disease;  
KW meningitis; diagnosis; treatment; ds.

XX Neisseria meningitidis.

XX Key Location/Qualifiers  
FH 1. -2124  
FT /\*tag= a  
FT /product= "LbpB"  
XX

PN W09909176-Al.

XX 25-FEB-1999.

XX 10-AUG-1998; 98WO-EP005117.

XX 15-AUG-1997; 97GB-00017423.

PR 05-FEB-1998; 98GB-00002544.

XX (UNUT-) RIJKSUNIV URECHT.

XX (TECH-) TECHNOLOGY FOUND TECHNOLOGIEBIOTICHTING ST.

XX Pettersson-Fernholm AM, Tommassen JPM;

PI WPI; 1999-190165/16.

XX P-PSDB; AAW93496.

XX New lactoferrin-binding protein B polynucleotides - obtained from  
XX Neisseria meningitidis, used to develop products for the diagnosis,  
XX prevention and treatment of neisserial disease, e.g. meningitis.

XX Claim 2; Page 105-109; 116pp; English.

XX This invention describes novel lactoferrin-binding protein B (LbpB)  
XX strains of Neisseria meningitidis. The products of this invention can be  
XX used for vaccinating humans against neisserial disease e.g. meningitis.  
XX Antibodies raised against the proteins of the invention can be used for  
XX diagnosing or treating neisserial disease in humans. The LbpB  
XX polypeptides can also be used for identifying compounds which inhibit the

XX Sequence 2124 BP; 663 A; 461 C; 541 G; 459 T; 0 U; 0 Other;

XX Query Match 72.0%; Score 1562.4; DB 2; Length 2124;

XX Best Local Similarity 84.5%; Fred. No. 0;

XX Matches 1835; Conservative 0; Mismatches 286; Indels 51; Gaps 5;

QY 1 ATGTGTAACCGAATTATGGCGGCAATTCCTGTGTGCGCTTACTTTTGGCATCTTGATC 60  
|||

DB |||  
QY 1 ATGTGTAACCGAATTATGGCGGCAATTCCTGTGTGCGCTTACTTTTGGCATCTTGATC 60  
QY 61 GCGCGCAATTTTCGGCGTGCAGCCTCTTGTGCAATCAAGCCGACCGCTACCCCGTCACT 120  
DB |||||  
QY 61 GCGCGCAATTTTCGGCGTGCAGCCTCTTGTGCAATCAAGCCGACCGCTACCCCGTCACT 120  
QY 121 TTCAAGTCTAAGAGAGTTCCCACTTCGCCCTCTGCCGGTCTTCGGTAGAAGAACCGCG 180  
DB |||||  
QY 121 TTCAAGTCTAAGAGAGTTCCCACTTCGCCCTCTGCCGGTCTTCGGTAGAAGAACCGCG 180  
QY 181 GTCACACGCGCGCTGCGGCAATGCGGCTGTTGAGACGGAATATTCGCTTTCA 240  
DB |||||  
QY 181 GTCACACGCGCGCTGCGGCAATGCGGCTGTTGAGACGGAATATTCGCTTTCT 240  
QY 241 CGTGAAGATGCGACGCGCAATTCGCCATAGCAAAACAAGCAGAGAAAGAGCTGTCGTTAAA 300  
DB |||||  
QY 241 GATAAGGATGCAATGATTTTCCAAATAGCAAAACAAGCAGAGAAAGAGCTGTCGTTAAA 300  
QY 301 GAAGGTGATGTTCTGTTTTTATA CGGTTCAAAAGAAATAA ACTTTCAACA ACTTTAAAAGC 360  
DB |||||  
QY 301 GAGGAAGATATCTCTGTTTTTATA CGGTTTCCAAAAGAGATCAACGTCAGCAGCTTAAAGAT 360  
QY 361 GAAATTCATAAACGTAATCTCTGAGCAGCAATTAACCATCGAATAATGAAAAA 420  
DB |||||  
QY 361 AAAATTCGTCACCAATCTCTACGCGCAAGCAATTAACCATCGAATAATGAAAAA 420  
QY 421 TATAATTCGTTGTCAGTCCGCTTATGCTTTTACTTAAATAAAGGAAAAAGATGAAAT 480  
DB |||||  
QY 421 TATGATTTATAATTTGTAGATGAGGTTATGTTATATACTAAAGACGGAAGATGAAAT 480  
QY 481 GAGAAACATCGGATGAAAGAGCTTTCTTAATCGTTTATGAGCTATGACGTTTGTATAT 540  
DB |||||  
QY 481 GAGTGGACTTCAAAATTTACAAGCAGTCTACCAACCGCTTGGTTATGACGCTTTGTATAT 540  
QY 541 TATCTCGGAGAACATCTTCCCAATCTTACGAGCGGCGGGAACGGTCAATATTCGCGC 600  
DB |||||  
QY 541 TATTCGAGAACATCTTCCCAATCTTACGAGCGGCGGGAACGGTCAATATTCGCGC 600  
QY 601 AACTGGCAATATATGACCGATGCCATAGCTCATCGGAGAGCTAA --GGGCGTTTCCAGT 657  
DB |||||  
QY 601 AACTGGCAATATATGACCGATGCCATAGCTCATCGGAGAGAGATGATCTTAAATAAT 660  
QY 658 GTGATTTGGGTATATACCATATATGATGTAATGAAATTTGGGCGAGCTTCTTATGAGCT 717  
DB |||||  
QY 661 GAAGATTTGGGTATATGCTTTTATAGCGTCAAAATGTCCGAGCAACTTCTTATGCTGCG 720  
QY 718 AGGATCGGATGCGCGGGAACATCTCCGCAATATACGTTTAAATTTTCGACAAAAA 777  
DB |||||  
QY 721 ACTGCGAGCACCGGAGGGAACATCTCCGCAATATACGTTTAAATTTTCGACAAAAA 780  
QY 778 AACTGGAAAGTAAAGTTGATTAAATAATCAGTATGTCAAAAAGAGAGATGATCTTAAATAAT 837  
DB |||||  
QY 781 ACTCTGAATGCAAGCTGATTAAAAATCAGTATGTGCAAAAGAGAGATGATCTTAAATAAT 840  
QY 838 CCACGTGACCATTTACACATTTACCGCAACATGAGCGGCAACCGCTTTACCGGAGTCC 897  
DB |||||  
QY 841 CCACGTGACCATTTACGACATTTACTGCAAAATTTGAGCGGCAACCGCTTTACCGGAGTCC 900  
QY 898 AAAGTTAGCACCGAGGTGAAGACGACACGCTGATTAAGATATTTGTTTTCATACC 957  
DB |||||  
QY 901 AAAGTTAAACAGAGGTGAAGACGATCACGCTGATTAAGATATTTGTTTTCATACC 960  
QY 958 GATGCGCATCAGCGCTTTGAGGCGGTTTTTTTGGCGCAATACCGAGAGAGCTTTCGCGGG 1017  
DB |||||  
QY 961 GATGCGCATCAGCGCTTTGAGGCGGTTTTTTTGGCGCAATACCGAGAGAGCTTTCGCGGA 1020  
QY 1018 CGGTTTATCATGTAACGACAAACAGCGTATTCGGCGTGTTCGAGCAAAACAAAAACAGAG 1077  
DB |||||  
QY 1021 CGGTTTATCATGTAACGACAAACAGCGTATTCGGCGTGTTCGAGCAAAACAAAAACAGAG 1080  
QY 1078 ACAGCAACGCATCAGATACAAATCTGCGCTCCGCTCTGGAACACACCAAAATCTTG 1137  
DB |||||  
QY 1081 ACAGCAACGCATCAGATACAAATCTGCGCTCCGCTCTGGAACACACCAAAATCTTG 1140

Qy	1138	GATTCTCTAAAAATTTCCGTTGTGACGAGCGACATGATGACCAATGCGCGTGAAGTTTGGCATTT	1197
Db	1141	GATTCTCTAAAAATTTCCGTTGTGACGAGCGAAGTGGTGAATAATCCCGACCGTTTGAAGGTT	1200
Qy	1198	TTCACTATGCGCCGATTTTGGTTCATCCCGACAAACTTCTTGTCTCGAAGGGCGTGAATTCCT	1257
Db	1201	TTCACTATGCGCCGATTTTGGTTCATCCCGACAAACTTCTTGTCTCGAAGGGCGTGAATTCCT	1260
Qy	1258	TTGCTTAGCCCAAGAGAAACCATCGAGCTTGC CGCAGCGCAGGAGAAATGACCATCCGTGCT	1317
Db	1261	TTGCTTAACAAAGAAACCAACCATCGATCTTTC CGCAGCGCAGGAGAAATGACCGTCCGTGCT	1320
Qy	1318	TGTTGCGATTTTCTGACCTATGTGAACCTCGGACGATATAAAACCGACCGCCCGCGCTC	1377
Db	1321	TGTTGCGACATTTTTCACCTATGTGAACCTCGGACGATATAAAACCGAACCGCCCGCGCTC	1380
Qy	1378	AAACCCGAAGCGCAGGATGAAGAGGATTC CGGACATTTGATTAATGCGCGAAGAAACCGAAGAC	1437
Db	1381	CAACCGAAGCGCAGGATGAAGAGGGGACGAAGAGGGTGTAGCGGTTGATAACGGTAAA	1440
Qy	1438	GAAATTTCCGAAGATGATACGGGGAAGATGAAGTACCGAAGACGAGGAGCTGAAGAA	1497
Db	1441	GAAA--GCCAAGACGAAATTCGGCGATGAAGAAGACACCGGAGA-----	1481
Qy	1498	ACCGAAGAGAAACTGATGAAGACGAAGAGGAAGAACCCGAAGAAACTGGAAGAAACTGAAA	1557
Db	1482	--CGAAGTCGTAGAGATGAAGACGAAGATGAAGACGAAGAGAAATCGAA-----GAA	1533
Qy	1558	GAAACTCAAGAAACTGAAGAAACTGAAGAAAACCTGAAGAAAANTGCGCGACAGAAAGAGGC	1617
Db	1534	GAACCTGAAGAAAGACTGAAGAGGAAGAAACCCGAAGAAATTTGCGGCAGAGAAGAGGC	1593
Qy	1618	AACGGCGGTTACGCGACATCTCTGCCACTCCCGAAGCCTTAAGCGCAGGACATCGAC	1677
Db	1594	AACGGCGGTTACGCGACATCTCTGCCACTCCCGAAGCCTTAAGCGCAGGACATCGAC	1653
Qy	1678	CTTTTCTGAAAAGTATCCGACGGCGGAAGCGACATTC CGCAAAATTGGAAGAACACGC	1737
Db	1654	CTTTTCTGAAAAGTATCCGACGGCGGAAGCGACATTC CAATAAACGGAACGGCGCAT	1713
Qy	1738	TATACCGGCACATTGGGAAGCGGTATCGGCGTGC CGGATGAAGAAAGCGCAACAGCTAGAT	1797
Db	1714	TATACCGGCACATTGGGAAGCGGTATCGGCGTATCGGATATCGGATAT-----	1753
Qy	1798	GGCACTAGCTCCATTCAAAAGGATAGCTATGCGAAATCAAGCGGCAAAAGCAGAAATTTGAC	1857
Db	1754	-GTGGTAGCTCCATTCAAAAGATAGCTATGCGAATCAGGGCGAAAGCAGAAATTTACC	1812
Qy	1858	GTTGATTTGGTGCAGAGTCGCTTTTCAGGTAAGTTGACAGAAAAAAATGATACACACCCC	1917
Db	1813	GTTGATTTCGAAGCGAAGACGGTGTCCGGAATGCTGACAGAAAAAAATGATACACACCCC	1872
Qy	1918	GCTTTTATATTTGAABAAGGTGTGATTTGATGGCNAACGGTTTCCACCGTTTTCGCGCGTACT	1977
Db	1873	GCTTTTATATTTGAAAAAGGTGTGATTTGACGGTAACCGTTTTCACCGTTTTCGCGCATACT	1932
Qy	1978	CGTGAAATGGTGTGATTTTCTCTGGGCAAGGTTTCGACTAATCCCAAGCTTTTAAAGCC	2037
Db	1933	CGGAGAACGGTATTGACCTTTCTGGCAGGGTTTCGACTAACCCGAGAAGCTTCAAGGC	1992
Qy	2038	AGTAATCTTCTGTAGAAGAGGATTTTATGTTCCGAGCGGCGAGAGTTGGGTGGTAAAT	2097
Db	1993	GACAACTCTTCTGTAAACAGCGGGCTTTTATGGCCCGCAGCGGAGAAATTTGGGCGGTAAAT	2052
Qy	2098	ATTATCGACAGTGAACCGGAAATTCGGCGTGGTATTTCGGTTCGAAAGAAAGATATGACGAG	2157
Db	2053	ATTATCGACAGCGACCGGAATTCGGTGGGTATTTCGGGCGGAAAAAGATGACAGGAG	2112
Qy	2158	GTGAAAAAATGA	2169
Db	2113	GCAACACCATGA	2124

RESULT 3  
ACA41945  
ID ACA41945 standard; DNA; 2226 BP.  
XX  
XX ACA41945;  
XX  
XX  
DT 19-JUN-2003 (first entry)  
XX  
XX Prokaryotic essential gene #23602.  
DE  
DE Antisense; ds; prokaryotic essential gene; cell proliferation;  
KW drug design; gene.  
KW  
OS Neisseria meningitidis.  
XX  
XX WO200277183-A2.  
XX  
XX  
XX 03-OCT-2002.  
XX  
XX 21-MAR-2002; 2002WO-US000107.  
XX  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362859P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
PA  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
PI  
XX WPI; 2003-029926/02.  
DR P-PSDB; ABU38075.  
DR  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 14; SEQ ID NO 29815; 1766pp; English.  
PS  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
CC prokaryotic essential genes. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published pct sequences



XX SQ Sequence 2226 BP; 701 A; 466 C; 566 G; 493 T; 0 U; 0 Other;

Query Match 67.0%; Score 1454.2; DB 7; Length 2226;  
Best Local Similarity 81.9%; Pred. No. 0;  
Matches 1742; Conservative 0; Mismatches 343; Indels 42; Gaps 4;

QY 1 ATGTGTAACCGAATTATGGCGGCAATGCTCTTGTGGCTTACCTTTTGGCAATCTGTGATC 60  
Db 1 ATGTGTAACCGAATTATGGCGGCAATGCTCTTGTGGCTTACCTTTTGGCAATCTGTGATC 60

QY 61 GGCGGCAATTTCCGCTGACGCTGTGTGCAATCAACGCGGACGCGGTACCTCCCGTCACT 120  
Db 61 GGCGGCAATTTCCGCTGACGCTGTGTGCAATCAACGCGGACGCGGTACCTCCCGTCACT 120

QY 121 TTCAAGCTAAGGACGTTTCCCACTTCGCCCCCTCGCGGCTCTCGGTAGAAACACACGCG 180  
Db 121 TTCAAGCTAAGGACGTTTCCCACTTCGCCCCCTCGCGGCTCTCGGTAGAAACACACGCG 180

QY 181 GTCAACGACGCGGCTGCGGTGGGCAATGGCGCTGTGAGACGGAATATGCTTTTCAT 240  
Db 181 GTCAACGACGCGGCTGCGGTGGGCAATGGCGCTGTGAGACGGAATATGCTTTTCAT 240

QY 241 CGTGAAGATGCGACGCAATTTCCGATAGCAAAACAAGCAGAAAGAAAGCTGCTGTTTAA 300  
Db 241 CGTGAAGATGCGACGCAATTTCCGATAGCAAAACAAGCAGAAAGAAAGCTGCTGTTTAA 300

QY 301 GAAGGTGATGCTGTTTTTATACGGTTCAAAAGAAATAAATCTTCAACAACTTAAAGC 360  
Db 301 GAAGGTGATGCTGTTTTTATACGGTTCAAAAGAAATAAATCTTCAACAACTTAAAGC 360

QY 361 GAAATTCATAACGTAATCTGAGCGAAGCATACCATCGGAATATGAAATATAAAAA 420  
Db 361 AAAAAATCATCAACCAATCTTAATGTAGAAATTAGGACATCAGAAAAATGAAAAATAAAAA 420

QY 421 TATAATTTATCGTTGTGTCAGTCCGCTTATCTGTTTACTTAAACGGAAGAGTGAAT 480  
Db 421 TATGTTTATGAAATTTAGATGCGAGTTATGTAATATCTACAAAGGGAAGAAATGAAAT 480

QY 481 GAGAAACATCGGATGAAAGCAGTTTCTAATCGTTTAGCTATGACGGTTTTGTATAT 540  
Db 481 GAGTGGACTTCAATATCAACGAGTTTACCTACCGGTTTGGTTATGACGGTTTTGTATAT 540

QY 541 TATCTCGGAGAACATCTTCCCATCTTTACCGAGCGGGAACGGTGAAATATTCGGC 600  
Db 541 TATTCGCGAGAACATCTTCCCATCTTTACCGAGCGGGAACGGTGAAATATTCGGC 600

QY 601 AACTGGCAATATATGACGATGCCATAGCTCATCGGAGAGGTAA--GGGGTTTCCAGT 657  
Db 601 AACTGGCAATATATGACGATGCCATAGCTCATCGGAGAGGTAA--GGGGTTTCCAGT 657

QY 658 GTGGAATTTGGGTTATACCAATATATGTTAATGAAATTTGGGCGAGCTTCTTATGAGCT 717  
Db 661 GAAGATTTGGGTTATATCGTTTATTAACGTCAAAATGTGCGAGCAACTTCTTATGCTGCG 720

QY 718 AGGATCCGATGCGCGGGAACATCTCTGCGCAATATACGGTTAATTTTCGACAAAAA 777  
Db 721 ACTCCGACGACCGAGAGGGAACATCTCTGCGCAATATACGGTTAATTTTCGTAAGAAA 780

QY 778 AACTCGAAGTAAATTTGATTAATAATCAGTATCTGCAAAAGAGAGATGATCCTTAAAT 837  
Db 781 ACTTTGACGGTAAATTAATTAATAATCAGTATCTGCAAAAGAAACCGATGAAAGAAA 840

QY 838 CCACTGACCAATTTCAACATPACCGCAACATGTCGCGCAACCGCTTTTACCGGAGTGCC 897  
Db 841 CCGCTGACCAATTTACGACATTTACTGCAACATTTGACGCGCAACCGCTTTTACCGGAGTGCC 900

QY 898 AAAGTTAGCAGCGAGGTGAAGACGCAACACCTGATTAAGAAATATTTGTTTTTCCATACC 957  
Db 901 AAAGTTAACACCGAGGTGAAGACGCAACACCTGATTAAGAAATATTTGTTTTTCCATACC 960

QY 958 GATCCGATACGCGCTTTGAGGGCGGTTTTTTTCGCGCATACGAGAGAGCTTTCGCGG 1017  
Db 958 GATCCGATACGCGCTTTGAGGGCGGTTTTTTTCGCGCATACGAGAGAGCTTTCGCGG 1017

Db 961 GATCCGATACGCGCTTTGAGGGCGGTTTTTTTCGCGCATACGAGAGAGCTTTCGCGG 1020  
QY 1018 CGGTTTTATCAATAACGACCAACAGCGGTATTTCCGCGCTGTTTCGAGCAACAAACAAACAGAG 1077  
Db 1021 CGGTTTTATCAATAACGACCAACAGCGGTATTTCCGCGCTGTTTCGAGCAACAAACAAACAGAG 1080

QY 1078 ACAGCAACGATCAGATACAAATCTCTGCGCTCGCGTCTGGAAAAACACACAAATCTTG 1137  
Db 1081 GCATCAACGATCAGATACAAATCTCTGCGCTCGCGTCTGGAAAAACACACAAATCTTG 1140

QY 1138 GATTCTCTAAAAATTTCCGTTGACGAGCGGCTGATGACCAATGCGCTTAACTTTGCCAAT 1197  
Db 1141 GATTCTCTAAAAATTTCCGTTGACGAGCGGCTGATGACCAATGCGCTTAACTTTGCCAAT 1200

QY 1198 TTCACTATGCCCCGATTTTGGTTCATCCGACAAAACTTCTTGTGCAAGGCGGTGAAATTCCT 1257  
Db 1201 TCCCTATGCCCCGATTTTGGTTCATCCGACAAAACTTCTTGTGCAAGGCGGTGAAATTCCT 1260

QY 1258 TTGTTAGCCAGAGAAAAACATGAGCTTTCGCGAGGAGGAAAAATGACCATCCGTGCT 1317  
Db 1261 TTGTTCAAGATATCTCAACCATCGATCTTCCGACGCGAGGAAAAATGACCGTCACTGCT 1320

QY 1318 TGTTCGATTTTCTGACCTATGTGAACCTCGAGCGGATAAAAACCGCGCCCGCGCTC 1377  
Db 1321 TGTTCGACCTTTTGTGAACTCGAGCGGATAAAAACCGCGCCCGCGCAAGT 1380

QY 1378 AAACCGAGGCGCAGGATGAAGA---GGATTTCGGAATTTGATTAATGCGGAGAAAGCGAA 1434  
Db 1381 AAACCAAGGCGGAGATGAAATTTCCGAAGATGAAATTTGTTGAAGCGAGGAAATGAA 1440

QY 1435 GACGA---AATTTTCGGAAGATGATAACGCGGAGAGATGAACTCACCAGAAAGAGAGCT 1491  
Db 1441 GAGGATTTGGTCGCTGAAGAGAAAAACACGGAAGACGAACTCGTAGAAGATGAAGACAGA 1500

QY 1492 GAAGAAACCGAAGAGAAACTGTATGAAGACGAAGAGAAACCCGAGAAACTGAGAA 1551  
Db 1501 GAAGAGACGAAGTTTCCGAAGATGGTAACTGAAGACGAAGAAAGAAATCGCGAAGAA 1560

QY 1552 ACTGAAGAAACTGAAGAAAACTGAAGAAAACTGAAGAAAAATCCCGACAGAA 1611  
Db 1561 GATGATGATGAAGCCGAGAGAGGAGGAAATTTGAAGAACCCGAGAAAGATCCCGAGAA 1620

QY 1612 GAAGGCAACGCGGCTTCAGGACGATCTCGGCCACTCGGAGAGCTTAAAGGCGAGGAC 1671  
Db 1621 GCGGCGGTGCGGCTTCAGACGCGCATCCCGCCGCTTCGGAAGCCCTTAAAGGCGAGGAC 1680

QY 1672 ATCGACCTTTTCTGAAAGGTATCCGACGCGGAGCGACATTTCCGCAAAATTTGAAAA 1731  
Db 1681 ATCGACCTTTTCTGAAAGGTATCCGACGCGGAGCGCGACATTTCCGCAAACTTGAANA 1740

QY 1732 GCAGCTATACCGGCACTTTGGGAAGCGGCTATCGCGGTGCGGATAGAAGGCGAAGCAG 1791  
Db 1741 GCAGCTATACCGGCACTTTGGGAAGCGGCTATCAGCAAAACCCATTCAATGGGATAAAG 1800

QY 1792 CTAGATGCGCACTAGCTCCATTCAAAAGATAGCTATCGGATCAGCGGCAAGAGAGAA 1851  
Db 1801 GCGGAT-----AAAAAGCGGCAAAAGCAGAA 1827

QY 1852 TTTGACGCTGATTTTGGTGGAGTTCGCTTTTCAAGTAAAGTTGACAGAAAAAATGATACA 1911  
Db 1828 TTTGACGCTGATTTTGGGAGAAATCGATTTTCGGAACGCTGACGGAAGAAACCGGTGTA 1887

QY 1912 CACCCGCTTTTATATTTAAAAAGGTGATGATGGCAACCGTTTCCACGCTTTTGGCG 1971  
Db 1888 GAAGCTGCTTTCTATATTTAAAAAGGTGATGATGGCAACCGTTTCCACGCGACAGCA 1947

QY 1972 CGTACTCGTGAATGTTGTTGTTTGTCTGCGGCAAGGTTTCGACTAATCCCAAGATTTT 2031  
Db 1948 CGCACTCGGATACCGGCATCAATCTTTTCGGGAAAATGGTTTCGACCAACCCCAAACTTC 2007

QY 2032 AAAGCCAGTAACTTCTCTGAGAGGAGGATTTTATGCTCCGAGCGGCGAGGATTTGGGT 2091  
Db 2008 CAAGCTAGTGTCTTCTGTTAGAGGAGGATTTTACGCGCCCGAGCGGAGGAATTTGGCG 2067







SQ	Sequence	349980 BP; 87189 A; 93501 C; 84627 G; 84663 T; 0 U; 0 Other;
	Query Match	62.7%; Score 1360.8; DB 3; Length 349980;
	Best Local Similarity	79.0%; Pred. No. 0;
	Matches 1721; Conservative	0; Mismatches 367; Indels 90; Gaps 5;
QY	1	ATGTGTAACCGAATTAATGGCGCATTTGCTCTGTTGGTCCCTTACTTTTGGCATCTTGCAATC 60
DB	99481	ATGTGTAACCGAATTAATGGCGCATTTGCTCTGTTGGTCCCTTACTTTTGGCATCTTGCAATC 99422
QY	61	GGCGGCAATTTCCGCGTGCAGCCGTTGTTGTAATCAACGCGCAGCGGTACCCCGTCACT 120
DB	99421	GGCGGCAATTTCCGCGTGCAGCCGTTGTTGTAATCAACGCGCAGCGGTACCCCGTCACT 99362
QY	121	TTCAAGTCTAAGACGTTTCCCACTTCCGCGCTGCTCCGCGGCTTTCGTTAGAAACACACCCCG 180
DB	99361	TTCAAAATCTAAGACGTTTCCCACTTCCGCGCTGCTCCGCGGCTTTCGTTAGAAACACACCCCG 99302
QY	181	GTCAACACGCGCGCTCGGTGGGCAATGGGCTGTTGAGACGGAATACGCTTTTCAT 240
DB	99301	GTCAACGCGCGCGCTCGGTGGGCAATGGGCTGCTCCAAAGGCGGAATATTTGCTTCCAT 99242
QY	241	CGTGAAGATGCGACGCGCAATTTCCGATAGCAAAACAGCAGAGAAAGCTGCTGTTTAAA 300
DB	99241	AAACNAGACGTTACGGAATTTCCGACAGCATCAGCAGGAGCATCTGCCGCTTAAA 99182
QY	301	GAAGGTGATGTTCTGTTTTTATACGTTTCAAAAGAAATAAATCAACTTCAACAACTTAAAGC 360
DB	99181	GAGAAGGATATCTCTGTTTTTAGACGTTACGCTGAGAAAGACAGGCTGACAAACTTAAAG 99122
QY	361	GAATTCATTAACGTAATCTGAGGCAAGCATTTACACATCGGAATCGGAATGAATATAAAA 420
DB	99121	AAATCAACACGAGTATCTGATGTGAGGCTTATCATCGAAAGAAAGAGAGAAAAA 99062
QY	421	TATTAATATCGGTTTGTGTCAGTCCGCTTATGTGTTTACTA-----AAAAACGGAAGAT 474
DB	99061	TATCAATATCAATTTGTCGTTGGGCTATGTGTTTACAGGCGGAGGAGGAAGATAT 99002
QY	475	GAATTTGAGAAACATCGGATGAAAGCAGTTTTCTAATCGTTTATGAGCGTTTT 534
DB	99001	GAAGAAAGAAAGACTTCTGATGTTAAGGAGTTTGTAAACGATTTAGTTATGACGGTTTT 98942
QY	535	GTATATATCTCGGAGAACATCTTCCCAATCTTTACGAGCGCGGCAACGTTGAATAT 594
DB	98941	GTATATATTTCCGAGAACGTCCTTCCCAATCTTTACGAGCGCGGCAACGTTGCAATAT 98882
QY	595	TCCGGCAACTGGCAATATATGACCGATGCCATAGTTCATCGAGAGGTAAAGGGGTTTCC 654
DB	98881	TCCGGTAACTGGCAATATATGACCGATGCCATAGTTCATCGGACGTTAAGCGGTTTCC 98822
QY	655	AGTGTGATTTGGTTTATACACATATATGTTAATGAAATTTGGGCGAGCTTCTTATGAG 714
DB	98821	AGTACGATTTGGGTTTATACACATATATGTTAATGAAATTTGGGCGAATCTTCTTATGAG 98762
QY	715	GCTAGGATCCGATGCGCGGAAACATCTCCGCAATATACGTTTATTTTCGACAA 774
DB	98761	GCTAGGATCCGACGACGAGGAAAGCATCTCCGCAATATACGTTTATTTGTAAC 98702
QY	775	AAAAACCTGGAAGTAAAGTTGATTAATAAATCAGTATGTCAAAAGA-----GAGAT 825
DB	98701	AAAACCTGAAATGGCAGCTGATTAATAAATCAGTATGTCGAAATAAAGTAAATCCAAAT 98642
QY	826	GATCTTAAATCACTGACCATTTTACAATTAACGCAACATTTGACGCGCAACCGCTTT 885
DB	98641	GAGCCCAAAAAACCGCTGACCATTTACGATTAACGCAACATTTGACGCGCAACCGCTTT 98582
QY	886	ACCGGATGCGCAAGTACGACGAGTGAAGACGCAACACGCTGATAAGATATTTG 945
DB	98581	ACCGGATGCGCAAGTACGACGAGTGAAGACGCAACACGCTGATAAGATATTTG 98522
QY	946	TTTTTCCATACCGATCGCGCTTACGCGCTTGGAGGCGGTTTTTTCGCGCATTAACGAGAA 1005
DB	98521	TTTTTCCATACCGATCGCGCTTACGCGCTTGGAGGCGGTTTTTTCGCGCATTAACGAGAA 98462

QY	1006	GAGCTTCCGCGGCGGTTTATCATGTAACAGCAACACAGCGTATTTCGCGTGTTCGAGGCAAA 1065
DB	98461	GAGCTTCCGCGGCGGTTTATCATGTAACAGCAACACAGCGTATTTCGCGTGTTCGAGGCAAA 98402
QY	1066	CAAAAACAGACAGACGAAACGATCAGATACAAATCCTGCCCTGCGCTCGGAAACAC 1125
DB	98401	CAAAAACAGACAGACGAAACGATCAGATACAAATCCTGCCCTGCGCTCGGAAACAC 98342
QY	1126	ACCAAAATCTTGGATTTCTTAAATAATTTCCGTTGACGAGGCGATGATGACCATGCGCGT 1185
DB	98341	ACCAAAATCTTGGATTTCTTAAATAATTTCCGTTGACGAGGCGATGATGACCATGCGCGT 98282
QY	1186	AAGTTTGCATTTCCATATGCGCGATTTTGGTTCATCCCGACAAACTTCTTTGCGAAGG 1245
DB	98281	GAGTTTGCATTTCCATATGCGCGATTTTGGTTCATCCCGACAAACTTCTTTGCGAAGG 98222
QY	1246	CGTGAATTTCTTGGTTAGCCAGAGAAACCATGAGCTTCCGACGCGCAGGAAATG 1305
DB	98221	CGTGAATTTCTTGGTTAGCCAGAGAAACCATGAGCTTCCGACGCGCAGGAAATG 98162
QY	1306	ACCATCCGTTGTTGCGATTTTCTGACCTATGTGAAACTCGAGCGGATATAAAACCGAC 1365
DB	98161	ACCATCCGACCTGCTGCGATTTTCTGACCTATGTGAAACTCGAGCGGATATAAAACCGAC 98102
QY	1366	CGCCCGCGCTCAAAACGAAAGCGCAGGATTAAGAGGATTCGGACATTTGATAATGCGCAA 1425
DB	98101	CGTCCCGCGCTCAAAACGAAAGCGCAGGATTAAGAGGATTAAGAGGATTAAGAGGATTCGGCGTT 98042
QY	1426	GAAGCGAAGACGAAATTTCCGAGATGATAACGCGGAGATGAGTTCACCGAAGAGAG 1485
DB	98041	GATAGCGTCAAGAA-----GGCGAAGACGAAATTCGACGATGAAGAA 98000
QY	1486	GAAGCTGAAGAAACCGAAGAACTGATGAAGACGAAAGGAAAGAACCCGAGAAACT 1545
DB	97999	GGCACCGAAGACCGCGCTTAAGACGAGGCGCAGCGAGAGCGAGCGATGAGAGGT 97940
QY	1546	GAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGCGCG 1605
DB	97939	GAA-----GATGAAGCTGAAGAACCCGAGAAAGAACTGCGCG 97904
QY	1606	ACAGAAAGGAAACCGCGGTTTCCGACGCGATCTCGGCGATCTCGGAGCGCTTAAAGGC 1665
DB	97903	ACAGAAAGGCGCGCGGTTTCCGACGCGATCTCGGCGCTCGGAGCGCTTAAAGGC 97844
QY	1666	AGGACATTCACCTTTTCTGAAAGGATTCGCGACGCGGAAAGCGACATTCGCAAAAT 1725
DB	97843	AGGACATTCACCTTTTCTGAAAGGATTCGCGACGCGGAAAGCGATTTCCGAAACT 97784
QY	1726	GGAAAGCAGCTATACCGGCACTTGGGAAAGCGGATTCGCGGTCGCGGATTAAGAAAGC 1785
DB	97783	GGAAAGCAGCTATACCGGCACTTGGGAAAGCGGATTCGCGGATTAAGAAAGC 97724
QY	1786	GAACAGCTAGATGCACTACGTCATTCATTAAGAGATAGCTATGCGATCAAGCGGCAAA 1845
DB	97723	AATCAGCGGAT-----AAAGAGCGGCAAA 97697
QY	1846	GCAGAAATTCGACGTTGATTTTGGTGGCAAGTTCGCTTTCAGGTAACTTGAAGAAAAAT 1905
DB	97696	GCAGTAATTCACGTTGATTTTGGCAAGAAATCGATTTCCGAAAGCTGACGAGGAAAC 97637
QY	1906	GATACACACCCCGCTTTTATATGAAAGGTTGATGATGGCAACGTTTCCAGCT 1965
DB	97636	GGTGTAGAACCTGCTTCCATATGAAACCGCAAGATTGAGGCAACGCTTCTACGCG 97577
QY	1966	TTGGCGGTACTCGTGAATGTTGATTTCTGTTGGCAAGTTTCGACTTAATCCCAA 2025
DB	97576	ACAGCAGCACTCGGAGAACCGCATCAATTTTCGGGAATGTTTCGACCGGACCCCAA 97517
QY	2026	AGTTTTAAAGCCAGTAACTTCTCGTAGAAGAGGAGATTTTATGTCGCGAGCGGAGAG 2085
DB	97516	ACCTTCCAGCTAGTAACTTCTCGTAGAAGAGGAGATTTTACGCGCGGAGGAGGAA 97457





Qy	1201	ACTATGCCCGCATTTTGGTCAATCCCGACAAACTCTCTTGTCCGAAGCGCGTGAATTCCTTTG	1261
Db	1264	CCTATGCCCGCATTTTGGTCAATCCCGACAAACTCTCTTGTCCGAAGCGCATGAATTCCTTTG	1323
Qy	1261	GTTAGCCGAAGAAAAACCTCCAGCTTCCGACGGCAGGAAATGACCATCCGTGCTTGT	1320
Db	1324	GTTAGCCGAAGAAAAACATCCAGCTTCCGACGGCAGGAAATGACCGCTCAGTGTCTGT	1383
Qy	1321	TGCGATTTTCTGACTATGTGAAACTCGGACGGATAAAAAACCGACCGCCCGCGCTCAAA	1380
Db	1384	TGCGACTTTTTCGACTATGTGAAACTCGGACGGATAAAAAACCGAACGCCCGCGCGCCAAA	1443
Qy	1381	CCGAAGCGCAGATGTAAGAGATTCCGACATGATTAATGCGCAAGAAAAACGCAAGACGAA	1440
Db	1444	CCGAAGCGCAGCAGGAAGAGATTCCGACATGATTAATGCGCAAGAAAAACGCAAGACGAA	1503
Qy	1441	ATTTTCCGAAGATGATAACGGCGAAGATGAGTCAACGAAGAGGAGAGCTGAGAAACC	1500
Db	1504	ATCGCGCATGAAAGAGAGGCACCGAAGATGACGCCGACGAGATGAAGCAGCGAAGAA	1563
Qy	1501	GAGAAGAAACTGATGTAAGACGAAGAGAAACCCCGAAGAACTGAAGAAACTGAAGAA	1560
Db	1564	GACGAAGCCACAGAAAACGAAGCGCGAAGAA	1596
Qy	1561	ACTGAAGAACTGAAGAAACTGAAGAAACTGAAGAAAAATTCGCGACAGAAAGGCAAC	1620
Db	1597	-----GACGAAGCTGAAGAACCTGAAGAGAAATCGTCG--GCAGAAGGCAAC	1641
Qy	1621	GGCGTTTCAGGCAGCATCTCGCCACCTCCCGAGCCCTTAAGCGAGGACATCGACCTT	1680
Db	1642	GGCAGTTTCAAACGCCATCTCTCGCTGTCCCGAAGCCCTTAAGCGAGGATATCGACCTT	1701
Qy	1681	TTCTGTAAGGTATCCGACAGCGGGAAGCCGACATTCGCAAAATTGGAAAAGCACGCTAT	1740
Db	1702	TTCTGTAAGGTATCCGACAGGCAGAAACGAATATTCGCAAACTGGAGAGACACGCTAT	1761
Qy	1741	ACGGCACTTTGGGAAGCGGTATCGGCGTCCCGGATAAGAAAGCGCAACAGCTAGATGC	1800
Db	1762	ACGGCACTTTGGGAAGCGGTATCGGCAAAACCCATTCAATGGGACAATCATCGGAT---	1818
Qy	1801	ACTACGTCCATTCAAAGGATAGCTATGCGAATCAAGCGCAAAAGCAGAAATTGACGTT	1860
Db	1819	-----AAGAAGCGCAAAAGCAGTATTTACCGTT	1848
Qy	1861	GAATTTTGGTTCGAAGTCGCTTTTCAGGTAACTTCACAGAAAAAATGATACACACCCGCT	1920
Db	1849	GAATTCGCAAGAAATCGAATTCGGAACGCTGACCGAGAAAAACGGTGTAGAACCTGCT	1908
Qy	1921	TTTTATNTGAAAAAGGTGTGATGATGCGAAACGGTTTCCACGCTTTGGCGCGTACTCGT	1980
Db	1909	TTCCGTAATGAAAAACGGCGTGATTGAGGGCAACGGTTTCCATGCGACAGCGCACTCGG	1968
Qy	1981	GAAAAATGGTCTGATTTGTCGGCAGGTTTCGACTAATCCCCAAAGTTTAAAGCCAGT	2040
Db	1969	GATGACGGCAATGCACCTTTCCGGCGAGGTTTCGACCAAAACCGCAGATCTTCAAAGTAAT	2028
Qy	2041	AATCTTCTCTAGAAGAGGATTTATGTGCCGAGCGCGCAGAGTTGGGTGTAATATT	2100
Db	2029	GATCTTCGTGTAGAAGGAGGATTTTACGGCCCGGAAGGCGGAGAAATGGCGCGTATATT	2088
Qy	2101	ATCGACAGTGAACCGAAA	2118
Db	2089	TTCAATAATGATGGAAA	2106

RESIST &amp;

RESULT 8  
AAX23322

AA23322  
ID AAX23322 standard: cDNA: 2262 BP.

XX  
77CC7VVV 7T

AX  
AC  
AAX23322:

HC  
XX  
AFAX23322;

11-JUN-1999 (first entry)

XXV

*N. meningitidis* strain M990 LbpB cDNA.

LbpB; lactoferrin binding protein; vaccine; neisserial disease; meningitis; diagnosis; treatment; ds.

*Neisseria meningitidis.*

Key	Location/Qualifiers
CDS	1..2262
	/*tag= a
	/product= "LbpB"

WO9909176-A1.

25-FEB-1999.

10-AUG-1998; 98WO-EP005117.

15-AUG-1997: 97GB-00017423.

13-AUG-1997; 97GB-00017423;  
05-FEB-1998; 98GB-00002544;

(UYUT-) RIJKSUNIV UTRECHT

(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.

Pettersson-Fernholm AM, Tommassen JPM:

WPI; 1999-190165/16.

P-PSDB; AAW93495.

New lactoferrin-binding protein B polynucleotides - obtained from *Neisseria meningitidis*, used to develop products for the diagnosis, prevention and treatment of neisserial disease, e.g. meningitis.

Claim 2; Page 98-102; 116pp: English.

This invention describes novel lactoferrin-binding protein B (LbpB) strains of *Neisseria meningitidis*. The products of this invention can be used for vaccinating humans against neisserial disease e.g. meningitis. Antibodies raised against the proteins of the invention can be used for diagnosing or treating neisserial disease in humans. The LbpB polypeptides can also be used for identifying compounds which inhibit the

Sequence 2262 BP; 698 A; 487 C; 590 G; 487 T; 0 U; 0 Other;

Query Match 57.7%; Score 1250.6; DB 2; Length 2262;

Best Local Similarity 76.9%; Pred. No. 7.8e-304;

MATCHES	1641;	Conservative	0;	Mismatches	429;	Indels	63;	Gaps	7;
---------	-------	--------------	----	------------	------	--------	-----	------	----

QY 1 ATGTGTAACCGAATTATGGCGCATTGTCTTGTTGCCCTTACTTTTGGCATCTTGCATC 60

7 7

THE UNIVERSITY OF CHICAGO

QY 61 GCGGCAATTTCGGCGTCAGCCTGTTGTCTGAATCAACGCCGACCGCG 108

Db 61 GCGGCAATTTCGGCGTACAGCCTGTTGTGGAATCAACGCCGCGCAACTCTGTCA 120

**C**

100 E

121

Db  
121 GATTCCAAATCTTCCAAATCCTGCGGATAAGCCTGCTCCAGCTCCTGCGAGCCTTCGGTA 180

169 GAAACCAAGCCGGTCAACCAAGCCCGCGTCGGTGGCAATGCGGCTGTTGAGACGGAAT 228  
QY

181 GAAATCAGCGCGTCAAGCGCGCGCGTGGGCAATGGGCTGCCAAGCGCGCAT 240

229 ACTGGCTTTTCATCGTGAAAGATGGCACGGCATAATCCCGATAGCGAACAACAGCAGACGAAAAAC 289

QY 229 AC TGC TTT TCA TCG TGA AGA TGG CAU GGC AA TCC CGA TAG CAA ACAAG CAG AAG AAG 288

349	Qy	CAACTTAAAGCGAAATTCATAAACGTPAATCCTGAGCGAAGCAFTACCACATCGGAAAT	408
361	Db	AAACTTAAAGGAAATCAACGGACGGCATCTAAATGCACAAATCTACACGTCGGATTTA	420
409	Qy	GAAATATAAATAATATTCGTTTGTTCAGTCCGGTTATCTGTTTACTTAAACCGGA	468
421	Db	AAAGATGATCGGTATCAATATAAATATGTCCGGCCGGATATGTTTATCTAGATATGGA	480
469	Qy	AAAGATGAAATTTGAGAAAAATCATCGGATGAAAAAGCAGTTTCTAATCTGTTAGGCTATGAC	528
481	Db	ACAGATGAAATTCGAACGAACTCAGGCGGTAAAGCGGTACCCACCGCTTAGGTTATGAC	540
529	Qy	GGTTTTCGTATATCTCGGAGAACATCTTCCCAATCTTTTACCGAGCGGGAAACGGTG	588
541	Db	GGTTTTCGTATATATTCGGGAGAACGTCCTTCCCAATCTTTTACCGAGTCGGGAAACGGTG	600
589	Qy	AAATATTTCCGGCAACTGGCAATATATGACCGATGCCATAGCTCATCGGAGAGGTAAAGGGG	648
601	Db	GAAATATCTGGTAACTGGCAATATATGACCGATGCCAAGCTCATCGAGCAGGTCAAGCG	660
649	Qy	GTTTTCAGTGTGGATTGGTTTATACACATATATATGCTAATGAAATGGGCGAGCTTCT	708
661	Db	GTTGGCAATGCAAAATTTGGTTATATCACATTTTATGGTAAACGATGTGTGTCGAACCTTCT	720
709	Qy	TATGAGGCTAGGGATGCCATATATGACCGATGCCAATAGCTCATCGGCAATATACGGTTAATTC	768
721	Db	TATCGGCTAAGATGTGCGAAGGAGAAAGCATCTCTGCCAATATACGGTTGATTTT	780
769	Qy	GACAAAAAAACCTGGAAGGTAACTTGATTAAAAATCAGTATGTGC--AAAAAGAGAGAT	825
781	Db	GATAACAAAAACATGAATGGCAAGCTGATTAATAATCAGTATGTGCGAAATATAAAAAAGAT	840
826	Qy	GATCCTAAAAATCCACTGACATTTTCAACATTAACCGCAATTCGACATGGACGCAACCGCTTT	885
841	Db	GAAACCAAAAAACCGCTGACCATTTTGCACATTACTGCAAAATTTGGACGCAACCGCTTT	900
886	Qy	ACCGGCAGTGCAAAAGTTAGCACCGAGGTGAAGACGCAACCGCTGATAAAGAATATTTTG	945
901	Db	ACCGGCAGTGCCAAAGTCAATCTCTGATTTAGCGAAAAAACCTTGCCGGTAATGAGCGTTTG	960
946	Qy	TTTTTTCCATACCGATCCGATCAGCGGCTTGAGGCGGTTTTTTCGCGGATACGCGAA	1005
961	Db	TTTTTTCCATGCGGATGCCGATCAGCGGCTTGAGGCGGTTTTTTCGCGGATACGCGAA	1020
1006	Qy	GAGCTTGCGGCGGTTTATCAGTAAACGACAAACAGCGTATTTGCGCGTGTTCGAGGCAAA	1065
1021	Db	GAGCTTGCGGACGGTTTATCAGCAACGACACACAGCGTATTTGCGCGTATTCGAGGCA--	1078
1066	Qy	CAAAAAACAGAGACAGCAACCGCATCAGATACAAATCTGCGCTTCGCGCTGCGAAACAC	1125
1079	Db	-AAAAAACAGAGACAGCAACCGCAGCAGATACAAACCTGCGCTTCGCGCTGCGAAACAC	1137
1126	Qy	ACCAAAATCTTGATTTCTTAAAAATTTTCGTTGACGAGCGACTGATACCATGCCCGT	1185
1138	Db	ACCAAAATCTTGATTTCTTAAAAATTTTCGTTGACGAGCGACTGATGCCATGCCCGT	1197
1186	Qy	AAAGTTGCAATTTCCATATGCGCCGATTTTGGTCAATCCGACAAACCTTCTGTCGAAGG	1245
1198	Db	AAAGTTGCAATTTCTCTATGCCGATTTTGGTCAATCCGACAAACCTTCTGTCGAAGG	1257
1246	Qy	CGTCABAATCTCTTGGTTTAGCCAGAGAAACCATCGAGCTTCGCGACGCGCAGAAATG	1305
1258	Db	CGTGAATTTCTTTGGTAAACGAAGAACAAATCATCAAGCTTCGCGACGCGCAGAAATG	1317
1306	Qy	ACCATCCGCTGCTTGTGCGATTTTTCACCTTATGTAAATCTCGGACCGGATAAAAAACCGAC	1365
1318	Db	ACCGTCCGCTGCTTGTGCGACTTTTTCACCTTATGTGAAATCTCGGACCGGATAAAAAACCGAT	1377
1366	Qy	CGCCCGCGCTCAAAACCGAAGCGCAGGATGAAGAGGATTCGACATTTGATATGCGGAA	1425
1378	Db	CGCCCGCGCAAGTAAACCAAAAGCGGAGATGAAGGGAGGATGAAGAGGTTGACGGCTT	1437
1426	Qy	GAAACGGAAGACGAAATTTTCGAGAGATGATAACGGCGAAGATGAAGTGAAGTCAACGAGAGAG	1485

[illegible]

## RESULT 9

AAA81482/C

AAA01402/C  
ID AAA81482 standard; DNA; 14652 BP.

AA  
AC  
AAA81482:

AA	04-DEC-2000	(first entry)
DT		

DE N. meningitidis partial DNA sequence qmm 30 SEO ID NO:30. XX

XX	
KW	<i>Neisseria meningitidis</i> ; <i>Neisseria gonorrhoeae</i> ; genome; immunogenic;
KW	antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW	<i>Meningococcus B</i> ; <i>MenB</i> ; ds.

XX  
OS  
Neisseria meningitidis.

AA  
PN  
WO200022430-A2.XX  
PD  
20-APR-2000

XX  
PF 08-OCT-1999: 99WO-US023573.

XX  
PR 09-OCT-1998: 98US-0103794P.

PR 09-OCT-1998; 98US-0103734E;  
PR 30-APR-1999; 99US-0132068P.

XX  
LX

(CHIR ) CHIRON CORP.

PA Frazier CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
 PI Rappuoli R, Pizza M;  
 XX  
 DR WPI; 2000-318079/27.

XX Isolated nucleotide sequences of *Neisseria meningitidis* which can be used  
 PT in the diagnosis and treatment of *N. meningitidis* infection and other  
 PT *Neisseria* infections, for example, *N. gonorrhoea*.  
 XX  
 PS Claim 7; Page 582-586; 1760pp; English.

XX The present invention describes methods of obtaining immunogenic proteins  
 CC from *Neisseria* genomic sequences. AAA81453 to AAA82414 represent  
 CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;  
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent *Neisseria* DNA  
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and  
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of  
 CC *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent  
 CC *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all  
 CC used in the exemplification of the present invention. The nucleic acid  
 CC sequences, protein sequences, and antibodies against them, can be used in  
 CC the manufacture of a composition. The composition can be used as a  
 CC medicament (or in the manufacture of a medicament) for treating,  
 CC preventing or diagnosing infection due to *Neisseria* bacteria. For  
 CC example, some of the identified proteins could be components of vaccines  
 CC against *Meningococcus B*; against all serotypes; and/or against all  
 CC pathogenic *Neisseriae*. Identification of sequences from the bacterium  
 CC will also facilitate production of biological probes, particularly  
 CC organism-specific probes. Attempts to make efficacious *Meningococcus B*  
 CC vaccines have failed mainly due to antigen tolerance. Multivalent  
 CC vaccines have also been tried but none have successfully overcome  
 CC antigenic variability. The provision of further, complete sequences may  
 CC provide an opportunity to identify secreted or surface exposed proteins  
 CC that may be presumed targets for the immune system and which are not  
 CC antigenically variable or at least more conserved than other more  
 CC variable regions  
 XX

SQ Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;

Query Match 40.0%; Score 868.2; DB 3; Length 14652;  
 Best Local Similarity 77.5%; Pred. No. 2.3e-207;  
 Matches 1141; Conservative 0; Mismatches 248; Indels 84; Gaps 4;  
 700 GCAGCTTCTATAGGCTAGGGATGCCGATGCCGCGGAAACATCTCCGGAATATACG 759  
 14652 GCACTTCTTATGAGGCTAGGGATGCCGATGCCGCGGAAACATCTCCGGAATATACG 14593  
 760 GTTAATTCGACAAAAAACCTCGAAGTTAAGTTGATTAATAATCAGTATGTGCAAAAG 819  
 14592 GTTGATTTGATAACAAACCTCGAATGGCAAGCTGATTAATAATCAGTATGTGCAAAAT 14533  
 820 A-----GAGATGATCTTAAAAATCCACTGCCATTTTACACATTACCGCAACATTG 870  
 14532 ABAAGTAATCCAATGAGCCCAAAAACCGCTGACCTTTACGACATTACCGCAACATTG 14473  
 871 GACGGCAACCGCTTTACCGGAGTGCCAAAGTTAGCACCGGAGTGAAGACCAACAGCT 930  
 14472 GACGGCAACCGCTTTACCGGAGTGCCAAAGTTAGCACCGGAGTGAAGACCAACAGCT 14413  
 931 GATAAAGAAATTTGTTTTCATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTTC 990  
 14412 GATAAAGAAATTTGTTTTCATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTTC 14353  
 991 GGCATACCGGAGAAAGCTTTGCCGCGGCTTTATCAGTAACGACCAACAGCGTATTCGGC 1050  
 14352 GGCATACCGGAGAAAGCTTTGCCGCGGCTTTATCAGTAACGACCAACAGCGTATTCGGC 14293  
 1051 GTGTTCCAGGCAACAAAAACAGACGACGAAACGATCAGATCAAAATCTTCGCCCTG 1110  
 14292 GTATTCCAGGCAACAAAAACAGACGACGAAACGATCAGATCAAAATCTTCGCCCTG 14233

QY 1111 CCGTCTGGAACACACACCAAAATCTTGATTTCTTAAATTTCCGTTGACGAGCGACT 1170  
 DB 14232 TCGTCTGGAACACACACCAAAATCTTGATTTCTTAAATTTCCGTTGACGAGCGACT 14173  
 QY 1171 GATGACCATGCCGTAAGTTTGGCAATTTCCATATGCGCGATTTTGGTTCATCCGCAAAA 1230  
 DB 14172 GATAAAATCCCGCTGAGTTTGGCAATTTCCATATGCGCGATTTTGGTTCATCCGCAAAA 14113  
 QY 1231 CTTCTTGTGCGAAGGCGTGAAATTCCTTTGTTAGCCAGAGAAACCATCAGCTTGC 1290  
 DB 14112 CTTCTTGTGCGAAGGCGTGAAATTCCTTTGTTAGAAACCAACCATCAGCTTGC 14053  
 QY 1291 GACGCGAAGAAATGACCATCCGTGCTTTGTTGCGATTTTCTGACCTATGTGAAATCGGA 1350  
 DB 14052 GATGTAAGAAACGACAAATCCGAACCTGCTGCGATTTTCTGACCTATGTGAAATCGGA 13993  
 QY 1351 CGGATAAAACCGACCGCCCGCTCAACCGAAGGCGCGAGATGAAGAGGATTCGGAC 1410  
 DB 13992 CGGATGCAACCGAACCGTCCCGCGCCAAACCGAAGGCGCGAGAGAGAGGAGCGAA 13933  
 QY 1411 ATTGATATGCGAAGAAAGCGAAGCAAAATTTCCGAAGATGATAACGCGCAAGATGAA 1470  
 DB 13932 GAGGATACAGCGGTTGATAGCTCGAAGAA-----GGCGAAGACGAA 13891  
 QY 1471 GTACCCGAGAGAGGAGCTGAAGAAACCGAAGAGAAACTGATGAAGACGAAGAGAA 1530  
 DB 13890 ATCGACGATGAAGAGCGCACCGAAGACGACCGCTTAAAGAGCAAGGCGAGAGAGAC 13811  
 QY 1531 GAACCCGAGAGAACTGAAGAAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACT 1590  
 DB 13830 GAACCCGTAGAAAGTGTAAGAT-----GAAGCTGAAGAAACCC 13795  
 QY 1591 GAAGAAAATCCGCGACAGAAAGGCAACCGCGGTTTCAGGACGATCTCTGCCACTCG 1650  
 DB 13794 GAAGAGAACTGCGACAGAAAGGCGGAGCGGTTTCAGCGGATCTCTGCCACTCG 13735  
 QY 1651 GAACCTCTAAGGCGAGGACATCGACCTTTCTGAAAGGTATCCGACGCGGAGAGCC 1710  
 DB 13734 GAACCCCTTAAAGCGAGGAAACATCGACCTTTCTGAAAGGTATCCGACGCGGAGAGCC 13675  
 QY 1711 GACATTCGCGAAATGGAAGAGCGCTATACCGGCACTTGGGAGGCGGATCGCGGTG 1770  
 DB 13674 GATATTCGGAACCTGAGAGAGCACTATACCGGCACTTGGGAGGCGGATCGCGCAA 13615  
 QY 1771 CCGGATAAGAAAGCGCAACGAGCTAGATGGCACTACGCTCCATTCAAAAGGATAGCTATCG 1830  
 DB 13614 CCAATTCATGGGACATCAGGCGAT----- 13588  
 QY 1831 AATCAAGCGCAAAAGCAGAAATTTGACGTTGATTTTGGTGCAGAGTCGCTTTCAGGTAAG 1890  
 DB 13587 AAAGAGCGCAAAAGCAGTATTTTACCGTTGATTTTCGCAAGAAATCGATTTCCGGAACG 13528  
 QY 1891 TTGACAGAAAATGATACACACCGCTTTTATTTATTTGAAAAGGTGATGATGAGG 1950  
 DB 13527 CTGACGAGGAAACCGGTGTAGAACCTGCTTCCATATTGAAAACCGCAAGATTTAGGGC 13468  
 QY 1951 AACGTTTCCACGCTTTGGCGCGTACTCTGTGAAAATGCGTGTGATTTGCTGGCAAGGT 2010  
 DB 13467 AACGTTTCTACGGGACAGCACGCACTCGGAGAAACCGCAATCAATCTTTCCGGAATG 13408  
 QY 2011 TCAGTAATCCCAAGTTTAAAGCCAGTAATCTTCTCGTAGAAGGAGGATTTATGTT 2070  
 DB 13407 TCAGCGACCCCAAAACCTTCCAAAGCTAGTAACTCTTCGTAGAGGGGATTTTACGGC 13348  
 QY 2071 CCGAGGCGCAGAGTTGGTGTGTAATATTATCGACAGTACCGGAAATTCGGGTGGT 2130  
 DB 13347 CCGAGGCGGAGAAATGGGCGGTATTTATTTTCAATAATGATGGGAAATCTCTTGTGATA 13288  
 QY 2131 TTCGTTGCCAAGAAAGATATGACGAGGAGGTGAA 2163  
 DB 13287 ACTGAAGTACTGAATAAAGTTGATGTTGAA 13255

RESULT 10  
ID AAA81815 standard; DNA; 707 BP.  
XX AC AAA81815;  
XX DT 04-DEC-2000 (first entry)  
XX DE N. meningitidis partial DNA sequence gnm\_362 SEQ ID NO:362.  
XX NEisseria meningitidis; Neisseria gonorrhoea; genome; immunogenic;  
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;  
KW Meningococcus B; MenB; ds.  
XX OS Neisseria meningitidis.  
XX PN WO200022430-A2.  
XX PD 20-APR-2000.  
XX PF 08-OCT-1999; 99WO-US023573.  
XX PR 09-OCT-1999; 98US-0103794P.  
XX PR 30-APR-1999; 99US-0132068P.  
XX PA (CHTR ) CHIRON CORP.  
XX PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
PI Rappuoli R, Pizza M;  
XX WIPI; 2000-318079/27.  
XX PT Isolated nucleotide sequences of Neisseria meningitidis which can be used  
PT in the diagnosis and treatment of N. meningitidis infection and other  
PT Neisserial infections, for example, N. gonorrhoea.  
XX PS Claim 7; Page 1606; 1760pp; English.  
XX CC The present invention describes methods of obtaining immunogenic proteins  
CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent  
CC specifically claimed Neisseria meningitidis genomic DNA sequences;  
CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA  
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and  
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of  
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent  
CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all  
CC used in the exemplification of the present invention. The nucleic acid  
CC sequences, protein sequences, and antibodies against them, can be used in  
CC the manufacture of a composition. The composition can be used as a  
CC medicament (or in the manufacture of a medicament) for treating,  
CC preventing or diagnosing infection due to Neisserial bacteria. For  
CC example, some of the identified proteins could be components of vaccines  
CC against Meningococcus B; against all serotypes; and/or against all  
CC pathogenic Neisseriae. Identification of sequences from the bacterium  
CC will also facilitate production of biological probes, particularly  
CC organism-specific probes. Attempts to make efficacious Meningococcus B  
CC vaccines have failed mainly due to antigen tolerance. Multivalent  
CC vaccines have also been tried but none have successfully overcome  
CC antigenic variability. The provision of further, complete sequences may  
CC provide an opportunity to identify secreted or surface exposed proteins  
CC that may be presumed targets for the immune system and which are not  
CC antigenically variable or at least more conserved than other more  
CC variable regions  
XX SQ Sequence 707 BP; 199 A; 155 C; 178 G; 173 T; 0 U; 2 Other;  
Query Match 22.7%; Score 491.6; DB 3; Length 707;  
Best Local Similarity 81.9%; Pred. No. 3.1e-113;  
Matches 579; Conservative 1; Mismatches 121; Indels 6; Gaps 1;  
QY 23 GCATTGCTGTGGCCCTTACTTTTGGCATCTTGGCATCGGCGCAATTCGGCGTCAGC 82

Db 1 GCATTGCTGTGGCCCTTACTTTTAGCATCTTGTATCGGCGCAATTCGGCGTCAGC 60  
QY 83 CTGTTGCGAATCAACCGCGACCGGTACCCCGTACCTTTCAAGTCTAAGACGTTCCCA 142  
Db 61 CTGTTGCGAATCAACCGCGACCGGTACCCCGTACCTTTCAAAATCTAAGACGTTCCCA 120  
QY 143 CTTGCCCCCTGCGGGTCTTTCGTAGAAACACGCGGTCAACCGCGCGCGCGTCCGCTG 202  
Db 121 CTCGCCCCCTGCGGGTCTTTCGTAGAAACACGCGGTCAACCGCGCGCGCGTCCGCTG 180  
QY 203 CGGCAATCGGCTGTTGAGACGGAATCTGCTTTTCATCGTGAAGATCGCAACGCAATTC 262  
Db 181 CGGCAATCGGCTGCGAAGCGGAATATTGCTTCTCTATAAACACAGCGGTACGGAATTC 240  
QY 263 CGATAGCAACAAGCAGAGAAAGCTGTGTTTAAAGAGGTGATGTTCTGTTTTTAT 322  
Db 241 CCGACAGCATCAGCAGAGGAGCATCTGCGCTTAAAGAGAGGATATCTGTTTTTAG 300  
QY 323 ACGGTTCAAAAGAAATAAACTTCAACAACTTAAAGCGAAATTCATAAACGTAATCCTG 382  
Db 301 ACGGTACGCTGAAGACAGCGCTGACAACTTAAAGAGAAATCAACGAGTATCTG 360  
QY 383 AGGCAAGCATTACCATCGGAAATGAAATATAAATAATAATTAATTCGGTTTGTGTCAGT 442  
Db 361 ATGTGAGGGTTATCACATCGAAAGAAAGAAAGAAATATCAATATCAATTTGTCCGTG 420  
QY 443 CCGGTTATGCTTTACTA- ----AAAACGGAAGATGAAATTCAGAAACATCGGATG 496  
Db 421 CCGGTATGTTTACCAGGCGGAAGAGGATATGAAAGAAAGAAAGATCTTCTGATG 480  
QY 497 AAAGCAGTTTCTAATCGTTTAGCTATGACGGTTTGTATATTTATCTCGGAGAACATC 556  
Db 481 GTAAGAGTTTGTAAACCGATTAGTTATGACGGTTTGTATATTTATTCGCGAGAACGTC 540  
QY 557 CTTCCCAATCTTACCGAGCGGGAACGTTGAATAATTCGCGCAACTGGCAATATATGA 616  
Db 541 CTTCCCAATCTTACCGAGCGGGAACGTTGCAATATTCGCGTAACTGGCAATATATGA 600  
QY 617 CCGATGCCATAGTCATCGGAGGTAAAGGGGTTTCCAGTGTGATTTGGGTTATACCA 676  
Db 601 CCGATGCCAAACGTCATCGGACANGTAAGGGCGGTTTCAGTACCGGATTTGGGTTATACCA 660  
QY 677 CATATTATGTAATGAAATTTGGGCGAGCTTCTTATGAGGCTAGGGAT 723  
Db 661 CATATTATGTAATGAAATTTGGGCGCACTTCTTATGAGGCTAGGGAT 707  
RESULT 11  
AAF91389  
ID AAF91389 standard; DNA; 1000 BP.  
XX AAF91389;  
AC AAF91389;  
XX DT 04-MAY-2001 (first entry)  
XX DE N. meningitidis (serogroup B) LbpA gene upstream sequence, SEQ ID:15.  
KW Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine;  
KW genetically modified; protective antigen expression; LPS detoxification;  
KW LPS; lipid A; homologous recombination vector; immunisation;  
KW immunoprotective; non-toxic; paediatric; cyclic; circular; ds.  
OS Neisseria meningitidis.  
XX PN WO200109350-A2.  
XX PD 08-FEB-2001.  
XX PF 31-JUL-2000; 2000WO-EP007424.  
XX PR 03-AUG-1999; 99GB-00018319.  
XX

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

Berthet FJ, Dalemans WLJ, Dencel P, Dequesne G, Feron C, Lobet Y;  
Poolman J, Thiry G, Thonnard J, Voet P;

WPI; 2001-138654/14.

New isolated polynucleotide useful for outer membrane vesicle preparation  
from Gram-negative bacterial strain for vaccination of microbial  
infections.

Claim 46; Page 81; 128pp; English.

The invention relates to a genetically-engineered outer membrane vesicle  
(bleb) preparation from a Gram-negative bacterium for use as a vaccine.  
The blebs of the invention are improved with respect to their  
immunogenicity and toxicity by the introduction of one or more genetic  
changes to the chromosome of the bacterium from which the blebs are  
derived. The changes made include the upregulation of protective antigen  
expression, the downregulation of immunodominant non-protective antigen  
expression, and genetic changes which result in detoxification of the  
Lipid A moiety of lipopolysaccharide (LPS). The invention also  
encompasses modified Gram-negative bacterial strains from which the bleb  
preparations are made, a vector suitable for performing recombination  
events (for the generation of the modified bacterial strains),  
bacterially-derived nucleic acid sequences used in such a vector, and an  
immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole  
cell vaccine suitable for paediatric use. The bleb preparation is useful  
in the manufacture of a medicament for immunising a human host against a  
disease caused by infection of one or more of the following: *Neisseria*  
*meningitidis*, *Neisseria gonorrhoeae*, *Haemophilus influenza*, *Moraxella*  
*catarrhalis*, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, and *Chlamydia*  
*pneumoniae*. The invention may also be used to provide immunisation against  
the influenza virus. Bacterially derived nucleotide sequences of the  
invention are used in the performance of homologous recombination events  
up to 1000 bp upstream of a bacterial chromosomal gene in order to either  
increase or decrease expression of that gene. Immunoprotective and non-  
toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more  
immunogenic, less toxic and safer, and are particularly useful for  
paediatric use. The present sequence represents a specifically claimed  
*Neisseria meningitidis* nucleic acid sequence

Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;

Query Match 20.2%; Score 439.2; DB 4; Length 1000;

Best Local Similarity 71.4%; Pred. No. 5.4e-100;

Matches 681; Conservative 0; Mismatches 203; Indels 70; Gaps 5;

QY	1210	GATTTTGGTTCATCCGACAAACTTCTTGTCGAGGGGCTGAAATTCCTTTGGTTAGCAA	1269
DB	1	GATTTTGGTTCATCCGACAACTTCTTGTCGAGGGGCTGAAATTCCTTTGGTTAGCAA	60
QY	1270	GAGAAACCCATCGAGTTGCGAGCGGAGGAAATGACCATCCGTGCTTGTGCGATTTT	1329
DB	61	GAGAAACCCATCGAGTTGCGAGCGGAGGAAATGACCATCCGTGCTTGTGCGATTTT	120
QY	1330	CTGACCTATGTAACCTCGGACGATTAACACCGACCGCCCGCTCAACCGAAGCG	1389
DB	121	TTGACCTATGTAACCTCGGACGATTAACACCGACCGCCCGCTCAACCGAAGCG	180
QY	1390	CAGGATGAAGAGGATTCGGACATTGATAATGGCGAAGAAAGGACGAAATTCGGAA	1449
DB	181	GAAGTAAAGGGA-----GGATGAAGAGATGCGAGC 213	
QY	1450	GATGATACCGCGAAGATGAAGTACCGAAGAGAGGAAGCTGAAGAAACCGAAGAGAA	1509
DB	214	GTGGTAACTCGAAGAG-----GCGAAGCGAAGTTCCGNAGATGAAGCGAAGAA	267
QY	1510	ACTGATCAAGACGAGAGGAGAACCCGAGAAACTGAAGAACTGAAGAACTGAAGAA	1569
DB	268	GCGAAGAAATCTGTCGAGAGAGAACCCGAGAAAGTGAAGAGGAAGAGCT---GAA	324
QY	1570	ACTGAAGAACTGAAGAACTGAAGAAATTCGCCGACAGAGNAGCGGCGGTCA	1629

DB	325	CCCAAGAGATTGAAGAAACCGAAGAAATCCGCCACAGAGAAAGCGGCGGTTCA	384
QY	1630	GGCAGCATCTCCCACTCCGGAAGCTCTTAAGGCGAGGACATCGACCTTTTCTGAAA	1689
DB	385	AACGCCATCTCTGCTCGGAGCCTCTAAGGCGAGGACATCGACCTTTTCTGAAA	444
QY	1690	GGTATCCGACGCGGGAAGCGGACATTCGCCAAATTTGAAAAAGCAGCTATATACCGCACT	1749
DB	445	GGTATCCGACGCGGGAAGCGGACATTCGCAAGAACCGGAAAGACACATATACCGCACT	504
QY	1750	TGGGAAGCGGATGTCGCGTCCGGAATGAAGAAAGCGAACAGCTAGATGGCACTACGTC	1809
DB	505	TGGGAAGCGGATGTCGCGTCCGCAACCCATTCATGGGACAATCAGGCGAT-----	552
QY	1810	ATTCAAAAGGATAGCTATGCGGATCAAGGCGCAAGGCAAGATTTGACGTTGATTTGGT	1869
DB	553	-----AAGAGCGGCAAAAGCAGATTTTACCCTTAATTTTCGGC	591
QY	1870	GCGAAGTCGCTTTCAGGTAAGTTGACAGAAAAAATGATACACCCCGCTTTTATATT	1929
DB	592	GAGAAATCGATTTCCGGAACGCTGACGGGAGAAACGGTGACACCTGCTTTCTATTT	651
QY	1930	GAAGAGTGTGATGATGGAACGGTTTCACGCTTTGGCGGCTACTCGTGAAGAGT	1989
DB	652	GAAGAGTGTGATGATGGAACGGTTTCACGCTTTGGCGGCTACTCGTGAAGAGT	711
QY	1990	GTTCATTTGTCGGGCAAGTTTCGACTAATCCCAAGTTTAAAGCCAGTAATCTTCTC	2049
DB	712	ATCAATCTTCGGGAATGGTTGACCAACCCAGACCTTCCAAAGCTAGTATCTCGT	771
QY	2050	GTAGAAGGAGGATTTTATGTTCCGCGGCGCAGAGTTGGGTGGTAAATATTATCGACAGT	2109
DB	772	GTAGAAGGAGGATTTTATGTTCCGCGGCGCAGAGTTGGGTGGTAAATATTATCGACAGT	830
QY	2110	GACCGGAAATTCGGGTGGTATTTCGGTCGGAAGAAAGATATGCGAGGAGTGGAA	2163
DB	831	GATCGGAAATCTCTTGGTATACTGAAGTACTGAAATAAAGTTGAAGTTGAA	884

RESULT 12

ABK37769

ID ABK37769 standard; DNA; 1000 BP.

XX ABK37769;

XX AC

DT 08-MAY-2002 (first entry)

XX DNA sequence upstream of LbpA #1 gene.

DE Upstream sequence; ds; Antibacterial; vaccine; bleb;

KW Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;  
meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;  
sinusitis.

OS *Neisseria meningitidis* serogroup B.

XX WO200209746-A2.

PN 07-FEB-2002.

PD 31-JUL-2001; 2001WO-EP008857.

XX 31-JUL-2000; 2000WO-EP007424.

PR 08-FEB-2001; 2001GB-00003170.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Berthet FJ, Dalemans W, Denoel P, Dequesne G, Feron C, Garcon N;  
PI Lobet Y, Poolman J, Thiry G, Thonnard J, Voet P;  
XX WPI; 2002-188688/24.

PT New immunogenic composition comprising an antigen derived from a pathogen  
PT and a blep preparation from *Neisseria meningitidis*, useful as a vaccine  
PT for treating or preventing disease caused by the pathogen.  
XX  
PS Disclosure; Page 84; 125pp; English.

XX The invention relates to an immunogenic composition comprising an antigen  
CC derived from a pathogen capable of protecting a host against the  
CC pathogen, mixed with an adjuvant comprising a blep preparation derived  
CC from a Gram-negative bacterial strain. The immunogenic composition  
CC consists of *N. meningitidis* B blebs or *N. meningitidis* C polysaccharide  
CC antigen. The blebs (derived from the outer membrane) may also have their  
CC toxic lipopolysaccharide (LPS) content reduced using heterologous down  
CC regulating sequences for LPS pathway genes or by up regulating genes  
CC involved in LPS synthesis suppression. By a promoter replacement  
CC technique. The immunogenic preparation is useful in the manufacture of a  
CC medicament for the treatment of a disease caused by the pathogen from  
CC which the antigen is derived (e.g. from *Neisseria meningitidis* and  
CC bacteraemia, from *Moraxella*, otitis media and pneumonia, and from *H.*  
CC *influenzae* chronic bronchitis, sinusitis, pneumonia and otitis media).  
CC The bleb derived from *M. catarrhalis* or from a non-typeable *H. influenzae*  
CC is useful as an adjuvant in an immunogenic composition comprising one or  
CC more pneumococcal capsular polysaccharides or protein antigens. The  
CC present sequence is an upstream sequence from an *N. meningitidis*,  
CC *H. influenzae* or *M. catarrhalis* gene involved in LPS biosynthesis, which  
CC either up regulates or down regulates sequences to which it is attached  
XX

SQ Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;

Query Match 20.2%; Score 439.2; DB 6; Length 1000;  
Best Local Similarity 71.4%; Pred. No. 5.4e-100;  
Matches 681; Conservative 0; Mismatches 203; Indels 70; Gaps 5;

QY 1210 GATTTGTCATCCCGACAACTTCTGTCGAAGGCGGTGAATTCCTTTGGTTAGCCAA 1269  
DB 1 GATTTGTCATCCCGACAACTTCTGTCGAAGGCGGTGAATTCCTTTGGTTAGCCAA 60  
QY 1270 GAGAAACCATGACCTGCGACGAGGAAATGACCATCGCTGTTGCGCATTT 1329  
DB 61 GAGAAACCATGACCTGCGACGAGGAAATGACCATCGCTGTTGCGCATTT 120  
QY 1330 CTGACCTATGTGAAGTCCGACGATATAAACCAGCCGCGCTCAAAACCGAAGCG 1389  
DB 121 TTGACCTATGTGAAGTCCGACGATATAAACCAGCCGCGCTCAAAACCGAAGCG 180  
QY 1390 CAGGATGAAGAGATTGCGACATTGATATGCGAAGAAAGCGAAGAGAAATTCGGA 1449  
DB 181 GAAAGTAAAGGGA-----GGATGAAGAGAGTGCAGGC 213  
QY 1450 GATGATACGGCGAAGATGAAGTCAACCGAAGAGGAGGAGCTGAAGAAACCGAAGAA 1509  
DB 214 GTTGTGAAGTGAAGAG-----GCGAAGGCGAAGTTTCCGAGATGAAGCGGAAGAA 267  
QY 1510 ACTGATGAAGACGAAGAGGAGAAACCGAAGAAACTGGAAGAACTGAAGAACTGAAGAA 1569  
DB 268 GCCGAGAAATCGTGAAGAGAAACCGAAGAGAGCTGAAGAGAGAACTGGAAGAA 324  
QY 1570 ACTGAAGAACTGAAGAACTGAAGAAATTCGCGACAGAGAGAGGCAACCGCGTTCA 1629  
DB 325 CCCAAAGAGTGAAGAAACCGAAGAAATTCGCGACAGAGAGAAACCGCGGCTTCA 384  
QY 1630 GCGAGCATCTGCCACTCCGAGAGCTCTTAAGGCGAGGAGCATGACCTTTTCGTGAAA 1689  
DB 385 AAGCCATCTGCTCTGCGAGAGCTCTTAAGGCGAGGAGCATGACCTTTTCGTGAAA 444  
QY 1690 GGTATCCGACGCGGAGCGGACATTCGCGAAATTTGGAAGACGCTATACCGCACT 1749  
DB 445 GGTATCCGACGCGGAGCGGACATTCGCGAAATTTGGAAGACGCTATACCGCACT 504  
QY 1750 TGGGAGCGGCTATCGCGTTCGCGATATGAAGAGCGGCACTAGCTAGCTAGCTCC 1809  
DB 505 TGGGAGCGGCTATCGCGACACCCATTCATGGGACAATCAGCGCAT-----552

QY 1810 ATTCAAAGGATAGCTATCGAATCAAGCGGCAAAAGCAGAAATTTGAGTTTGGT 1869  
DB 553 -----AAAGAGCGCAAAAGCAGAAATTTACGTTAAATTCGCG 591  
QY 1870 GCGAAGTGCCTTTTCAGGTAAGTTCACAGAAAAAATGATACACCCCGCTTTTATATT 1929  
DB 592 GAGAAATCGATTTCGCGAAACGCTGACGAGAGAAAAACGGGTACAACTGCTTCTATATT 651  
QY 1930 GAAAAAGTGTGATGATGCGCAACGGTTTCCACGCTTTGGCGCTACTCGTGAAATCGT 1989  
DB 652 GAAAAACGCGAAGATTGAGGGCAACGGTTTCCACGCAACAGCAGCAGCTCGTGAGAACGC 711  
QY 1990 GTTGATTTGCTCGGCAAGGTTCCACTAATCCCAAGTTTAAAGCCAGTAATCTCTC 2049  
DB 712 ATCAATCTTTTCGGAATGGTTCCACCACCCAGAACCTTCCAGCTAGTGATCTCGT 771  
QY 2050 GTAGAAGAGAGATTATGTTGTCGCGAGCGCGCAGAGTTGGTGTTATATTATCAGACT 2109  
DB 772 GTAGAAGAGAGATTATGTTGTCGCGCGCA-CGCGAGGAAATTTGGCGGTATTTTTCATTAAG 830  
QY 2110 GACCGGAAAAATCGGCTGTTATTCGGTCCGAGAAAGATATGCGAGGAGTGGAA 2163  
DB 831 GATGGGAAATCTCTTGGTATTAACCTGAGGTACTGAAATATAAGTTGAAGTTGAA 884

RESULT 13

AAS75460  
ID AAS75460 standard; cDNA; 400 BP.

XX AC AAS75460;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #11264.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX P-PSDB; ABG11273.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX Claim 1; SEQ ID NO 11264; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging









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Best Local Similarity 4.9%; Pred. No. 3.1e-13;
Matches 19; Conservative 239; Mismatches 128; Indels 0; Gaps 0;

QY 1268 AAGAGAAACCATCGAGCTTCCGACGCGAGGAAATGACCATCGCTGTTGCGGATT 1327
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1416 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1357
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1328 TTCTGACATGTAAGAACTCGGACGATAAAACCGACGCGCCCGCTCAACCGAAG 1387
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1356 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1297
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1398 CCAGATGAAGAGATTCGGACATGATAATGCGAAGAACCGAAGCAAGAAATTCG 1447
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1296 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1237
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1448 AAGATGATAACCGCGAAGATGAAGTCAACGAGAGAGAACTGAAGAAACCGAAG 1507
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1236 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1177
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1508 AAAGTGAAGAGAGAGAGAACCGGAGAGAACTGAAGAAACTGAAGAACTGAAG 1567
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1176 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1117
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1568 AAAGTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAG 1627
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1116 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1057
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1628 CAGGAGCATCTCGCCACTCGGAA 1653
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1056 CCTCGACCTGACGCAAGCTCGAA 1031
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-363 : polymorphic base A or G
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-363.mis1, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-454-363.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 139..158
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind

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; LOCATION: 634..652
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-454-363 potential probe
; NAME/KEY: misc feature
; LOCATION: 674..679,881..882,892..893
; OTHER INFORMATION: n=a, g, c or t
; US-09-671-317-14

Query Match 3.9%; Score 85.4; DB 4; Length 929;
Best Local Similarity 60.3%; Pred. No. 1.1e-13;
Matches 149; Conservative 0; Mismatches 96; Indels 2; Gaps 1;

QY 1372 GCCGTCAACCCGAGGCGCAGGATCAAGAGATTCGGACATTCGGAATTAATCGCGAAGAACG 1431
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 909 GCACCTCCAGCCTGAGCNCAGCAGGANNCCATCTCAAGAGAGAGAGAGAGAGAGAGAA 850
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1432 GAAGACGAAATTTCCGAAAGATGATAACCGCGAAGATGAAGTCAACGAGAGAGAGAGAGAG 1491
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 849 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1492 GAAGAAACCGAAGAGAGAACTGATGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 789 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1552 ACTGAGAGAACTGAGAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA 1611
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 731 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1612 GAAGGCA 1618
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 671 GAAGAA 665

RESULT 3
US-09-671-317-439/c
; Sequence 439, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 439
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-242 : deletion AT
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-242.mis1, potential
; NAME/KEY: primer_bind
; LOCATION: 260..279
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind

```



```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match
Best Local Similarity 3.4%; Score 73.4; DB 3; Length 43795;
Mismatches 128; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1378 AAACCGAGGCCGAGGATGAGAGGATTCGGACATGTAATGCGCGAAGAAAGCGAAGAC 1437
Db 38833 AAAAAAAAAAAAAAAAAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 38892
QY 1438 GAAATTTCCGAAGATGATAACCGCGAAGATGAAGTCAACCGAAGAGAGGAACTGAAGAA 1497
Db 38893 GGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 38952
QY 1498 ACCGAGAGAGAACTGATGAGAGACGAGAGAGAGAACCCGAGAGAACTGAAGAACTGAA 1557
Db 38953 AAGGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 39012
QY 1558 GAACTGAGAACTGAGAACTGAGAACTGAGAACTGAGAA 1596
Db 39013 GAAGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCA 39051

RESULT 6
US-08-766-738-2
; Sequence 2, Application US/08766738
; Patent No. 5916749
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,738
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0177 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 1813361
US-08-766-738-2

Query Match
3.3%; Score 72.6; DB 2; Length 966;
Best Local Similarity 58.9%; Pred. No. 2e-09;
Matches 128; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match
Best Local Similarity 3.4%; Score 73.4; DB 3; Length 43795;
Mismatches 128; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1378 AAACCGAGGCCGAGGATGAGAGGATTCGGACATGTAATGCGCGAAGAAAGCGAAGAC 1437
Db 38833 AAAAAAAAAAAAAAAAAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 38892
QY 1438 GAAATTTCCGAAGATGATAACCGCGAAGATGAAGTCAACCGAAGAGAGGAACTGAAGAA 1497
Db 38893 GGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 38952
QY 1498 ACCGAGAGAGAACTGATGAGAGACGAGAGAGAGAACCCGAGAGAACTGAAGAACTGAA 1557
Db 38953 AAGGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 39012
QY 1558 GAACTGAGAACTGAGAACTGAGAACTGAGAACTGAGAA 1596
Db 39013 GAAGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCA 39051

RESULT 7
US-09-262-610-2
; Sequence 2, Application US/09262610
; Patent No. 6428949
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/262,610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0177 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 1813361
US-09-262-610-2

Query Match
3.3%; Score 72.6; DB 4; Length 966;
Best Local Similarity 58.9%; Pred. No. 4.1e-10;
Matches 123; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match
Best Local Similarity 58.9%; Pred. No. 4.1e-10;
Matches 123; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1387 GCGCAGGATGAGAGGATTCGGACATGTAATGCGCGAAGAAAGCGAAGCAATTTCC 1446
Db 571 GAGGTGGATGGTGTGTTGATNAAGANGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 630
QY 1447 GAAGATGATAACGGCGAAGATCAACTCACCGAAGAGAGGAGCTGAAGAAACCGAAGAA 1506
Db 631 GACGATGAGGATGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 690
QY 1507 GAAATCTGATGAGAGACGAGAGAGAGAACCCGAGAGAACTGAAGAACTGAAGAACTGAA 1566
Db 691 GAAGGGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 750
QY 1567 GAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAA 1595
Db 751 GAAGATGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 779

Query Match
3.3%; Score 72.6; DB 4; Length 966;
Best Local Similarity 58.9%; Pred. No. 4.1e-10;
Matches 123; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match
Best Local Similarity 58.9%; Pred. No. 4.1e-10;
Matches 123; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1387 GCGCAGGATGAGAGGATTCGGACATGTAATGCGCGAAGAAAGCGAAGCAATTTCC 1446
Db 571 GAGGTGGATGGTGTGTTGATNAAGANGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 630
QY 1447 GAAGATGATAACGGCGAAGATCAACTCACCGAAGAGAGGAGCTGAAGAAACCGAAGAA 1506
Db 631 GACGATGAGGATGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 690
QY 1507 GAAATCTGATGAGAGACGAGAGAGAGAACCCGAGAGAACTGAAGAACTGAAGAACTGAA 1566
Db 691 GAAGGGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 750
QY 1567 GAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAACTGAGAGAA 1595
Db 751 GAAGATGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 779
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 11:49:00 ; Search time 4949.35 Seconds  
(without alignments)  
13086.780 Million cell updates/sec

Title: US-10-735-098-3

Perfect score: 2169

Sequence: 1 agtgtaaacgaattatgg.....tcgaggaggtgaaaaatga 2169

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	103.6	4.8	879	28	AZ550718
C 2	103.6	4.8	881	28	AZ688514
C 3	103.6	4.8	942	28	BH148582
C 4	102.6	4.7	434	14	CA745444

5	100.4	4.6	675	28	BZ104011
6	100.2	4.6	665	13	BU432980
7	99.8	4.6	264	13	BQ241566
8	99.8	4.6	686	29	CE063557
9	99	4.6	612	28	BZ149404
10	98.8	4.6	575	10	BF707975
C 11	98.6	4.5	232	29	CG321416
C 12	98.6	4.5	880	28	AZ529191
C 13	98.4	4.5	265	14	CA607797
C 14	97.8	4.5	263	13	BQ005139
15	97.6	4.5	689	28	AZ971991
16	97.6	4.5	960	28	CC143364
17	97.2	4.5	622	13	BU418103
C 18	97	4.5	233	12	BJ454017
19	97	4.5	332	14	CA566759
C 20	96.6	4.5	311	14	CA699402
21	96.6	4.5	340	13	BQ462203
C 22	96.6	4.5	739	28	BZ220379
23	96.2	4.4	871	29	CG354013
24	95.6	4.4	395	29	CE760553
25	95.6	4.4	558	12	BM163267
C 26	95.4	4.4	289	14	CA716220
27	95.4	4.4	617	14	CA743799
28	95.2	4.4	453	12	BM167376
29	95.2	4.4	459	12	BM171330
30	95.2	4.4	648	12	BM164042
31	95.2	4.4	739	12	BM160442
32	95.2	4.4	753	12	BM167115
33	95.2	4.4	790	12	BM166415
34	95.2	4.4	900	28	AZ549980
35	95.2	4.4	925	28	AZ538036
36	95.2	4.4	1030	14	CF470007
37	95	4.4	531	14	CD915362
C 38	95	4.4	546	28	AZ600777
39	94.8	4.4	799	28	BZ201507
40	94.6	4.4	596	29	CC660549
C 41	94.6	4.4	691	28	BH040136
42	94.6	4.4	953	13	BQ939407
43	94.4	4.4	617	14	CD925518
C 44	94	4.3	1096	14	CK206118
C 45	93.8	4.3	421	28	AZ113646

#### ALIGNMENTS

RESULT 1  
AZ550718/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ550718 879 bp DNA linear GSS 14-NOV-2000  
ENTEM36TF Entamoeba histolytica Sheared DNA Entamoeba histolytica  
genomic, genomic survey sequence.

AZ550718 GI:11176019

GSS

Entamoeba histolytica

Entamoeba histolytica

Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 879)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HMI:IMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjloftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared

DNA library

Seq primer: M13-Forward

Class: shotgun

High quality sequence start: 25  
High quality sequence stop: 801.

```

FEATURES
source
Location/Qualifiers
1..879
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica"
/notes="Vector: pHOSt1; Site 1: Bat
Institute for Genomic Research (T
Genomic DNA isolated from broth c
using a method described by Clar
C.G., and Diamond, L.S. (1993) E
method for isolate identification
7:450.). The DNA was mechanically
tight size distribution (~2 kb).
the library construction is desc
H.O. and Venter, J.C. (Making sm
whole genome shotgun sequencing
Sequencing: A Practical Approach,
Barell. Oxford University Press.

```

## ORIGIN

	Query Match	4.8%;	Score 103.6;	DB 28;	Length 879;
	Best Local Similarity	64.7%;	Pred. No. 6.5e-11;		
	Matches 154;	Conservative 0;	Mismatches 84;	Indels 0;	Gaps 0;
QY	1393	GATGAAGAGATTCCGACATGTAAATGGCGAAGAAGCAGACGAAATTTCCGAAGAT	1452		
Db	628	GACGAAGAAGATGNTGAAGAGAGATGAAGAGATCAAGAAGATGAAGAAGTGAAGAA	569		
QY	1453	GATAACGGCGAAGATGAAGTTCACGGAAGAAGAGGAAGCTTGAGAAACCGGAAGAAAAC	1512		
Db	568	GATCAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATCAAGAAGATGAAGAAGATCAA	509		
QY	1513	GATCAAGACCAGAGGAAGAACCCGGAAGAAACTGAAGAAAACCTGAAGAAAAC	1572		
Db	508	GAAGATGAAGAAGATGAAGAAGACGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGAT	449		
QY	1573	GAAGAACTGAAGAAACTGAAGAAAAATGCCCGACAGAGAAGGCACCGCGGTTCCAG	1630		
Db	448	GAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGA	391		

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RESULT 2
AZ688514/c
LOCUS
DEFINITION      881 bp      DNA      linear      GSS 14-DEC-2000
                  ENTMU22TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
                  genomic, genomic survey sequence.
ACCESSION      AZ688514
VERSION        AZ688514.1  GI:11825660
KEYWORDS
SOURCE
ORGANISM      Entamoeba histolytica
                Entamoeba histolytica
                Eukaryota; Entamoebidae; Entamoeba.
                1 (bases 1 to 881)
AUTHORS      Loftus,B., Van Aken,S. and Fraser,C.
TITLE        Determination of clone end sequences from Entamoeba histolytica
                HML:IMSS sheared DNA library
JOURNAL
COMMENT      Unpublished (2000)
                Contact: Brendan J Loftus
                Department of Eukaryotic Genomics
                The Institute for Genomic Research
                9712 Medical Center Dr., Rockville, MD 20850, USA
                Tel: 301 838 0208
                Fax: 301 838 3543
                Email: bjlloftus@tigr.org
                Clones are derived from the Entamoeba histolytica HML:IMSS sheared
                DNA library
                Seq primer: M13-Forward
                Class: shotgun
                High quality sequence start: 15

```

High quality sequence stop: 765.  
Location/Qualifiers

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1. .881
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: pHO81; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, I.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barelli, Oxford University Press, 1999)."
```

ORIGIN

Query Match	4.8%;	Score 103.6;	DB 28;	Length 881;
Best Local Similarity	64.7%;	Pred. No. 6.5e-11;	Indels 0;	Gaps 0;
Matches 154;	Conservative 0;	Mismatches 84;		

```

Qy 1393 GATGAAGAGATTCCGACATTGTATATGGCGAAGAAGCGAAGACGAATTTCCGAAGAT 1452
Db 300 GACGAAGAAGATGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAA 241

Qy 1453 GATTAACGGCGAAGATGAAGTACCAGGAAGAAGACGAGCTGAAGAAACCGAAGAAGAACT 1512
Db 240 GATGAAGAAGATGAAGAAGAATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAA 181

Qy 1513 GATGAACACCAAGGAAGAAGACCCGAAGAAACTGAAGAAACTGAAGAAACTGAAGAAACT 1572
Db 180 GAAGTGAAGAAGATGAAGAAGACGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGAT 121

Qy 1573 GAAGAAACTGAAGAAACTGAAGAAAAATCCCGACAGAAAGACGACCGCGTTTCAG 1630
Db 120 GAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAG 63
```

## ORIGIN

	Query Match	4.8%;	Score 103.6;	DB 28;	Length 881;
	Best Local Similarity	64.7%;	Pred. No. 6.5e-11;		
	Matches 154;	Conservative	0;	Mismatches 84;	Indels 0; Gaps 0;
Qy	1393	GATGAAGAGATTCCGACATTTGATATGGCCGAAGAAGCGAAGACGAAATTTCCGAAGAT	1452		
Db	300	GACGAAGNAGAGATGNTGAAAGAGATGAAGAGATCAAGAAGATGAAGAAGATGAAGAA	241		
Qy	1453	GATAACGGCGAAGATGAAGTTCACCGAAGAAGAGGAGCTGTAAGAAACCGAAGAGAAACT	1512		
Db	240	GATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAA	181		
Qy	1513	GATCAACACCAAGGGAAGAACCCGGAAGAACTTGAGAAAATCTGAAGAAATCTGAAGAAACT	1572		
Db	180	GAAGTGAAGAAGATGAAGAAGACGAAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGAT	121		
Qy	1573	GAGAAACTGAAGAAACTGAAGAAAAATCCCGACACGAAGAAGCAACGCGGTTCTAG	1630		
Db	120	GAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGAAG	63		

RESULT 3	BH148582	942 bp	DNA	linear	GSS 27-AUG-2001
LOCUS	BH148582	ENTP262TF	Entamoeba histolytica	Sheared DNA	Entamoeba histolytica
DEFINITION	BH148582	genomic, genomic survey sequence.			
ACCESSION	BH148582				
VERSION	BH148582.1	GI:15308029			
KEYWORDS	GSS.				
SOURCE	Entamoeba histolytica				
ORGANISM	Entamoeba histolytica				
REFERENCE	Eukaryota; Entamoebidae; Entamoeba.				
AUTHORS	1 (bases 1 to 942)				
TITLE	Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.				
JOURNAL	Determination of clone end sequences from Entamoeba histolytica				
COMMENT	HM1:IMSS sheared DNA library (2001)				
	Unpublished (2001)				
	Contact: Brendan J Loftus				
	Department of Eukaryotic Genomics				
	The Institute for Genomic Research				
	9712 Medical Center Dr., Rockville, MD 20850, USA				
	Tel: 301 838 0208				
	Fax: 301 838 3543				
	Email: bilofus@tigr.org				
	Clones are derived from the Entamoeba histolytica HM1:IMSS sheared				
	DNA library				
	Seq primer: M13-Forward				
	Class: shotgun				
	High quality sequence start: 15				
	High quality sequence stop: 794.				





Site 2: NotI; This normalized library was constructed from 1.1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Ronaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match	4.6%;	Score 100.2;	DB 13;	Length 665;
Best Local Similarity	65.3%;	Pred. No. 3.2e-10;		
Matches 147;	Conservative 0;	Mismatches 78;	Indels 0;	Gaps 0;
QY	1391	AGGATGAAGAGGATTCCGACATTGATTAATGGCCGCAAGAAAGCGAAGACGAAATATTCGGAAG	1450	
Db	196	AGAGTGAAGATGNAGATGAAGAGAGATGAAGAAGATGAAGAAGAGCGAAGATG	255	
QY	1451	ATGATTAACGGCGAAGATGAAGTCCACGGAAGAGAGGAAGACTGNAGAAAACGGAAGAGAAA	1510	
Db	256	ACCAAGAGAGATGAAGATGAAGATGAAGAAGAAGATGAAGATGACGTGACGAAGAAGAAG	315	
QY	1511	CTGATGAAGACGAAGAGGAGAAACCCGAAGAAACTGAAGAAACTGAAGAAACTGGAAGAAA	1570	
Db	316	AGATGAAGAGAGAGATGAAGATGAAGAGAGAGATGAAGAAGATGAAGATGAAGATG	375	
QY	1571	CTGAAGAAACTGAAGAAACTGAAGAAAAATCCCGCACAGAAGAG	1615	
Db	376	ACGAAGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGATGAAGAAGAAG	420	

RESULT 7

B0241566

LOCUS

## DEFINITION

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ACCESSION  
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VERSION  
KEYWORDS

**RELATIONSHIP  
SOURCE**

ORGANIS.

11

## REFERENCES

## FEATURES

CONFIDENTIAL

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/organism="Triticum aestivum"  
/mol_type="mRNA"  
/cultivar="Glenlea"  
/db_xref="taxon:4565"  
/clone="TaE05003807R"  
/tissue_type="developing seeds"  
/dev_stage="5 days after anthesis"
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/db_xref="taxon:10116"
/clone="CH230-227E5"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/notes_vector="pTARAC2.1; Site 1: EcoRI;
CHORI-230 Rat (BN/SSNhd/MCW) BAC library produced by
Pieter de Jong"

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## ORIGIN

[illegible]

## RESULT 6

BU432980

LOCUS

## DEFINITION

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ACCESSION  
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**KEYWORDS**  
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ORGANIS

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## REFERENCES

## AUTHORS

TABLE

Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

nos



[illegible]

RESULT 10					
BF707975					
LOCUS	BF707975	575 bp	mRNA	linear	EST 12-JUN-2002
DEFINITION	A634 LE Aplysia metacerebral cell cDNA library Aplysia californica CDNA 5' , mRNA sequence.				

ACCESSION BF707975  
VERSION BF707975.1 GI:18002301  
KEYWORDS EST.  
SOURCE Aplysia californica (California sea hare)  
ORGANISM Aplysia californica

Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea; Aplysioidea; Aplysiidae; Aplysia.

REFERENCE  
1 (Bases 1 to 575)  
AUTHORS  
Sadreyev, R.I., Meleshkevich, E.A., Matz, M.V., Panchin, Y.V. and

TITLE	MOROZ, L. L.
Characterization of the gene pool expressed in the individual identified neuron	

JOURNAL  
COMMENT

University of Florida  
9505 Ocean Shore Blvd., St Augustine, FL 32080, USA

Tel: 904 461 4044  
Fax: 904 461 4008  
Email: [sadreyev@whitney.ufl.edu](mailto:sadreyev@whitney.ufl.edu)

FEATURES	Location/Qualifiers	seq primer: 5' CGACGTGGACTATCCATGAACGCA 3'.
source	1..575	

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1. 373 /organism="Aplysia californica"  
/mol_type="mRNA"
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/db_xref="taxon:6500"
/tissue_type="nervous system"
/cell_type="Metacerebral cell"

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/clone_lib="Aplysia metacerebral cell cDNA library"
/note="Vector: pGEM-T"

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Query Match: 4.6%; Score 98.8; DB 10; Length 575;

Best Local Similarity 64.3%; Pred. No. 6.2e-10;  
Matches 148; Conservative 0; Mismatches 82; Indels 0; Gaps 0

1386 GGCGCAGGATGAAGAGGATTCGGACATGATATGGCGAAGAAAGCGAAGACGAAATTTTC 1441

[illegible][illegible]

OY 1506 AGAAACTGTATGAAGACCGAAGGAGAACCCGNAAGA ACTGAAGAAA CTGAAGAACTGA 156

[illegible]

RESULT 11	CG321416	232 bp	DNA	linear	GSS 26-AUG-2003
LOCUS	CGYB153TV ZM 0.7-1.5 KB				
DEFINITION	Zea mays genomic clone ZMMBMa0640J09, genomic survey sequence.				

ACCESSION	CG321416
VERSION	CG321416.1
GI	34238682

KEYWORDS  
GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
1 (bases 1 to 232)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Nienisch, K., Pearson, C.M., Budman, M.A., Bedell, J.A., Rohlfing, T.,

**TITLE**  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics

JOURNAL COMMENT  
Unpublished (2002)  
Other\_GSSs: OGYB153TH  
Contact: Cathy Whitelaw

CONTACT: CECILY MULLER  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843  
Fax: 301-838-0208  
Email: [whitelaw@tigr.org](mailto:whitelaw@tigr.org)

Seq primer: TF  
Class: sheared ends.  
Location/Qualifiers

```

FEATURES
  source
    location/qualifiers
      1. .232
        /organism="Zea mays"

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/mol_type="genomic DNA"  
/strain="B73"  
/db_xref="taxon:4577"
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/clone="ZNMEMA0640J09"  
/clone_lib="ZM 0.7 1.5 KB"  
/clone_intron="pcgv_site 1. HincII. 0.7-1.5 kb
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ORIGIN
methylation filtered genomic DNA library"
/notes=vector: pvecsk; site: 11; name: 11;

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Best Local Similarity 64.9%; Pred. NO. 6.3e-10;

Matches 146; Conservative 0; Mismatches 79; Indels 0; Gaps 0

QY	1391	AGATGAGAGAGGATTCGGACATTAATAAGCGAAGAATCCGAAGCACTTCCCTTT
D6	232	AAGAAGAGAAGAAAGAAAGATGAAGAGAAGAGAAGAGAAGAGAAGAAGAAG

QY 1451 ATGATACGGCGGAGATGAAGTCCCGAAGAGGAGCTGAAGAAACCGAAGAGAA 1511

[illegible][illegible]

QY 1571 CTGAAGAAACTGAAGAAATCGCCCGACAGAAGAAG 1615

Db  
52 AAGAAGACGAAGAAGAAAGAAAGAAAGAAAGAAAG

RESULT 12  
A7529191/C

LOCUS	ENTB68TR	Entamoeba histolytica	880 bp	DNA	linear	GSS 03-NOV-2001
DEFINITION	ENTB68TR	Entamoeba histolytica	880 bp	Sheared	DNA	Entamoeba histolytica

genomic, genomic survey sequence.

ACCESSION AZ529191  
 VERSION AZ529191.1 GI:11081835  
 KEYWORDS GSS.  
 SOURCE Entamoeba histolytica  
 ORGANISM Entamoeba histolytica  
 Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 880)  
 Loftus B., Van Aken, S. and Fraser, C.  
 Determination of clone end sequences from Entamoeba histolytica  
 HM1:IMSS sheared DNA library  
 Unpublished (2000)  
 Contact: Brendan J Loftus  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0208  
 Fax: 301 838 3543  
 Email: bjloftus@tigr.org  
 Clones are derived from the Entamoeba histolytica HM1:IMSS sheared  
 DNA library  
 Seq primer: M13-Reverse  
 Class: shotgun  
 High quality sequence start: 17  
 High quality sequence stop: 673.

FEATURES  
 source  
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 /organism="Entamoeba histolytica"  
 /mol\_type="genomic DNA"  
 /strain="HM1:IMSS"  
 /db\_xref="taxon:5759"  
 /clone\_lib="Entamoeba histolytica Sheared DNA"  
 /note="Vector: pHOS1; Site 1: Bst I; Constructed at The  
 Institute for Genomic Research (TIGR), Rockville, MD.  
 Genomic DNA isolated from broth cultures of E. histolytica  
 using a method described by Clark and Diamond (Clark,  
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a  
 method for isolate identification. Exp. Parasitol.  
 77:450.). The DNA was mechanically sheared to give a  
 tight size distribution (~2 kb). The v + i method used for  
 the library construction is described in detail in Smith,  
 H.O. and Venter, J.C. (Making small insert libraries for  
 whole genome shotgun sequencing projects. In Genome  
 Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barel, Oxford University Press, 1999)."

ORIGIN  
 Query Match 4.5%; Score 98.6; DB 28; Length 880;  
 Best Local Similarity 64.9%; Pred. No. 7e-10;  
 Matches 146; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1391 AGGATGAGAGGATTCGACATTGATATCGCGAAGAAAGCGAGACGAAATTCGGAAG 1450  
 Db 698 AAGACGAGCGAGCGAAGATGACGAGAGAGCGAGAGACGAGAGAGAGAGCGAAG 639

QY 1451 ATGATACCGCGAAGATGAGTCACTCCGAGAGAGAGGAGCTGAAGAACCGAGAGAA 1510  
 Db 638 AAGAGAGAGCGAG 579

QY 1511 CTGATGAGAGCGAAGAGAGAAACCCGAGAGAACTGAAGAACTGAAGAA 1570  
 Db 578 AAGATGAGAGCGAAGAGATGAGACGAGAGAGAGATGAGACGAGAGAGATGAGACGAG 519

QY 1571 CTGAGAACTGAGAACTGAAGAAATTCGCGACAGAGAGAG 1615  
 Db 518 ATGATGAGAGCGAAGATGATGAGACGAGAGATGATGAGAGCGAAG 474

RESULT 13  
 CA607797/c  
 LOCUS  
 DEFINITION wrl.pk0082.f4 wrl Triticum aestivum cDNA clone wrl.pk0082.f4 5'

genomic, genomic survey sequence.

ACCESSION CA607797  
 VERSION CA607797.1 GI:25162959  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 265)  
 Tingey S.V., Powell W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
 Miao, G., Caraher, N. and Hanafey, M.K.  
 Dupont Wheat cDNA Sequence  
 Unpublished (2002)  
 Contact: Scott V. Tingey  
 Crop Genetics  
 E. I. DuPont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingey@USA.dupont.com  
 Seq primer: M13.

FEATURES  
 source  
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 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4565"  
 /clone\_lib="wrl.pk0082.f4"  
 /tissue\_type="root"  
 /clone\_lib="wrl"  
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:  
 XhoI; Wheat (Triticum aestivum L.) root; 7 day old  
 seedling, light grown"

ORIGIN  
 Query Match 4.5%; Score 98.4; DB 14; Length 265;  
 Best Local Similarity 62.7%; Pred. No. 7e-10;  
 Matches 141; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1391 AGGATGAGAGGATTCGACATTGATATCGCGAAGAAAGCGAGACGAAATTCGGAAG 1450  
 Db 240 AAGATGATGTTGAGNTGACGANGTGAAGANAGAGAGAGAGAGAGAGAGAGATG 181

QY 1451 ATGATACCGCGAAGATGAGTCACTCCGAGAGAGAGAGAGCTGAAGAACCGAGAGAA 1510  
 Db 180 AAGAAGATGAG 121

QY 1511 CTGATGAGAGCGAG 1570  
 Db 120 AAG 61

QY 1571 CTGAGAGAACTGAAGAAATTCGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615  
 Db 60 ANGAAG 16

RESULT 14  
 BU005139/c  
 LOCUS  
 DEFINITION QG7D20.yg.ab1 QG\_EFGHJ lettuce serriola lactuca sativa cDNA clone

ACCESSION BU005139  
 VERSION BU005139.1 GI:22439534  
 KEYWORDS EST.  
 SOURCE Lactuca sativa  
 ORGANISM Lactuca sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
 Cichorieae; Lactuca.

REFERENCE 1 (bases 1 to 263)  
 Kozik, A., Michalmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
 Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,

Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compgenomics.ucdavis.edu/  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]  
singleton, see http://cpgdb.ucdavis.edu/ for details.  
Plate: QGS7 row: D column: 20.  
FEATURES  
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/mol\_type="mRNA"  
/cultivar="L.serriola"  
/db\_xref="taxon:4236"  
/clone="QGS7D20"  
/lab\_host="E.coli"  
/clone\_lib="QG EFGHJ lettuce serriola"  
/note="Vector: pBRCDNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transfections made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cpgdb.ucdavis.edu/TAG\_SEQ-Not found"

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0245 row: M column: 07  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 689.  
FEATURES  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0245M07"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 4.5%; Score 97.6; DB 28; Length 689;  
Best Local Similarity 59.3%; Pred. No. 1.1e-09;  
Matches 166; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 1340 TGAAACTCGACGGATATAAAACCGACCGCCGCCCTCAACCGAGGCGCGGATGAAG 1399  
Db 2 TGNATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61  
QY 1400 AGGATTCGACATTGATATGGCGAAGAAAGCGAAGCAATTCGAGAGTATAACG 1459  
Db 62 AGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121  
QY 1460 GCGAAGTGAAGTACCGAAGAGAGGAGTCAAGAAACCGAAGAGAACTGATGAAG 1519  
Db 122 AGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181  
QY 1520 ACCAAGAGGAGAAACCCGAGAACTGAAGAAACTGAAGAAACTGAAGAACTGAAGAA 1579  
Db 182 AGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241  
QY 1580 CTGAAGAACTGAAGAAATCCCGACAGCAAGGCA 1619  
Db 242 AAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 281

Query Match 4.5%; Score 97.8; DB 13; Length 263;  
Best Local Similarity 63.3%; Pred. No. 9.4e-10;  
Matches 150; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1379 AACCGAAGCGGAGGATGAGGAGGATCGGACATTCATATGCGGAGGAGGAGGAGGAG 1438  
Db 263 AACAGACAGAAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 204  
QY 1439 AAATTTCCGAGATGATACGGCGAAGATGAAGTCAACCGAAGAGGAGGAGGAGGAG 1498  
Db 203 AAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 144  
QY 1499 CCGAAGAGAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1558  
Db 143 AAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 84  
QY 1559 AAATGAGAACTGAGAACTGAGAACTGAGAACTGAGAACTGAGAACTGAGAACTGAG 1615  
Db 83 AAGACGAAGAAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 27

RESULT 15  
AZ971991  
LOCUS 689 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0245M07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0245M07 R, genomic survey sequence.  
ACCESSION AZ971991  
VERSION 1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 689)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb









QY 61 GCGGCAATTTCCGCGTGCAGCTGTTGTGCAATCAACGCCGACCGCGTACCCCGTCACT 120  
Db 61 GCGGCAATTTCCGCGTGCAGCTGTTGTGCAATCAACGCCGACCGCGTACCCCGTCACT 120  
QY 121 TTCAAGTCTAAGAGGTTCACACTCCGCCCTCCGCGTCTTCGCTAGAAACACGCGC 180  
Db 121 TTCAAGTCTAAGAGGTTCACACTCCGCCCTCCGCGTCTTCGCTAGAAACACGCGC 180  
QY 181 GTCAACACGCGCGTCCGCTGCGGCAATGCGGTGTTGAGACGGAATPACTGCTTTTCAT 240  
Db 181 GTCAACACGCGCGTCCGCTGCGGCAATGCGGTGTTGAGACGGAATPACTGCTTTTCAT 240  
QY 241 CGTGAAGTGCACGGCAATTCGCGATAGCAAAACAGCAGAGAAAGCTGCTGTTTAAA 300  
Db 241 CGTGAAGTGCACGGCAATTCGCGATAGCAAAACAGCAGAGAAAGCTGCTGTTTAAA 300  
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QY 361 GAAATTTCAATAACGTAATCTGAGGCAAGCAATACCATCGGAAATGAAATATAAAAA 420  
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QY 421 TATAATTTATCGGTTGTCAGTCCGCTTATGTTTACTATAAACCGGAAGATGAAAT 480  
Db 421 TATAATTTATCGGTTGTCAGTCCGCTTATGTTTACTATAAACCGGAAGATGAAAT 480  
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Db 481 GAGAAACATCGGATGAAAGCAGTTTCTAATCGTTAGGCTATGACGTTTTCATAT 540  
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Db 541 TATCTCGGAGAACATCTTCCAAATCTTTACCGAGCGGGAAACGCTGAAATATTCGCG 600  
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Db 601 AACTGGCAATATGACCGATGCCATACGTATCGGAGAGTTAAGGGGTTCCAGTGTG 660  
QY 661 GATTTGGGTTATACCAATATTTATGTAATGAAATTTGGGCGAGCTTCTTATGAGCTAG 720  
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QY 781 CTGGAAGTTAAGTTGATTAATAATCAGTATGTCRAAAGAGAGATGATCCTTAAATCCA 840  
Db 781 CTGGAAGTTAAGTTGATTAATAATCAGTATGTCRAAAGAGAGATGATCCTTAAATCCA 840  
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QY 961 GCGGATCAGGGCTTCAGGGCGGTTTTTCGGCGATAACCGAGAGAGCTTCCGGCGG 1020  
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QY 1021 TTTATCAGTAAACGACACGCTATTTCCGCGTTCGCGGCAAAACAAAAACAGAGACA 1080  
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QY 1081 GCAACCGCATCAGATACAAATCTGCGCTGCGGTAACACACGCAAAATCTTGGAT 1140  
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QY 1381 CCGAAGCGCAGGATGAAGAGATTGCGACATTTGATTAATGCGGAAGAAAGCGAGACAA 1440  
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Db 1861 GATTTTGTGCGAAGTTCGCTTTGCTGCGCAAGGTTGCACTAAATCCCCAAAGTTTAAAGCCAGT 1920  
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Db 2041 AATCTTCTAGAGAGGAGATTTTATGTCGCGAGCGGCGAGAGTTGGTGGTAAATTT 2100  
QY 2101 ATCGACAGTGCAGGAAATCGCGGTGTTATTCGGTGCAGAAAGATATGACGAGAGGTG 2160  
Db 2101 ATCGACAGTGCAGGAAATCGCGGTGTTATTCGGTGCAGAAAGATATGACGAGAGGTG 2160  
QY 2161 GAAAAATGA 2169  
Db 2161 GAAAAATGA 2169

## RESULT 2

```

US-10-735-098-9
; Sequence 9, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain 881607
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2121)
US-10-735-098-9

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Query Match	72.0%;	Score 1562.4;	DB 17;	Length 2124;
Best Local Similarity	84.5%;	Pred. No. 0;		
Matches 1835;	Conservative 0;	Mismatches 286;	Indels 51;	Gaps 5;
QY	1	ATGTGTAACCGCAATTATGCGGCAATGTCCTGTTGGCCCTACTTTTGGCATCTTGCAATC	60	
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QY	61	GGCGGCAATTTCCGGCGTGCAGCCCTGTTGTCGAATCAACGGCGACCGCGTACCCCGTCACT	120	
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QY	121	TTCAAGTCTAAGAGACGTTTCCCACTTCGCCCCCTGCCGGGTCTTCGGTAGAACAACACGCCG	180	
DB	121	TTCAAGTCTAAGAGACGTTTCCCACTTCGCCCTCTGCCGGGTCTTCGGTAGAACAACACGCCG	180	
QY	181	GTCAACAGACCCCGCTCGGTGCGGCAATCGCGCTGTGTAGAGCGGAATCTGCTTTTCAT	240	
DB	181	GTCAACAGACCCCGCTCGGTGCGGCAATCGCGCTGTGTAGAGCGGAATCTGCTTTTCAT	240	
QY	241	CGTGAAGATGGCACGGCAATTCGGATAGCAAAACAGACGAGAAAAGCTGTCGTTTAAA	300	
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DB	301	GAGGAAGATATCTGTTTTTATACGTTCCAAAAAGATCAACGTGACGACCTTTAAGAT	360	
QY	361	GAAATTCATAACGTAATCTGTAGGCAAGCATTTACACATCGGAAATGAAAATAAAAAA	420	
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QY	421	TATAATATTCGGTTTGTTCAGTGCCGTTATGTGTTTTACTAAAAACGGAAGATGAAAT	480	
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QY	541	TATCTCGGAGACATCCTTCCCAATCTTTACCGAGCGCGGGAACCGGTGAAAATATTCGCGC	600	
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QY	601	AACTGGCAATATATAGACCCGATGCCATATACGTATCGGAGAGGTAA---GGGGTTTCCAGT	657
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QY	658	GTGGATTGGGTATATACACATATATATGGTAAATGAAATTGGGGCAGCTTCTTTATGAGCCT	717
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DB	721	ACTGCCGACGACCGGGAGGGAACATCTCCGCGAATATACGGTTAAATTTCGACAAAAA	780
QY	778	AACTGTGAAGTAAAGTTGATTTAAAAAATCAGTATATGCAAAAGCAGAGATGATCTCTAAAAAT	837
DB	781	ACTCTGAATGCAAGCTGATTAAAAAATCAGTATATGCAAAAGCAGAGATGATCTCTAAAAA	840
QY	838	CCACTGACCAATTACACATTTACCGCAACATTTGACCGGAAACCGCTTTTACCGGACGTGCC	897
DB	841	CCACTGACCAATTACGACATTTACTTCGCAAAATTTGACCGCAACCGCTTTTACCGGACGTGCC	900
QY	898	AAAGTTAGCACCGGAGGTGAAGACCAACACGCTGATAAAGAAATATTTGTTTTTCCATACC	957
DB	901	AAAGTTAAACAGAGGTGAAGACGAATCAAGCTGATAAAGAAATATTTGTTTTTCCATACC	960
QY	958	GATGCCGATCAGCGGCTTGAGGGCGGTTTTTTTCGGCGATAACGAGAAAGCTTGC CGG	1017
DB	961	GATGCCGATCAGCGGCTTGAGGGCGGTTTTTTTCGGCGATAAAGGGGAGAGCTTGC CGA	1020
QY	1018	CGGTTTATCAGTAACGACAACAGGGTATTTCCGGGTGTTTCGACGGCAACAAAAACAGAG	1077
DB	1021	CGGTTTATCAGCAACGACAACAGCGTATTTCCGGGTGTTTCGACGGCAACAAAAACAGAG	1080
QY	1078	ACAGCAAAACGATCAGATACAAATCTTCGCCCTCCGCTCTGGAAAAACACACCAAAATCTTG	1137
DB	1081	ACAGCAAAACGATCAGATACAAATCTTCGCCCTCCGCTCTGGAAAAACACACCAAAATCTTG	1140
QY	1138	GATTCTCTAAAAATTTCCGTTGACGAGGGGACTGATGACCATGCCCGTAAGTTTGCAATT	1197
DB	1141	GATTCTCTAAAAATTTCCGTTGACGAGGCAAGTGGTGAATAATCCCGACCGTTTGAGTT	1200
QY	1198	TCCACTATGCCCAATTTTGGTCAATCCGCAAAACTCTTTGTTCGAAGGGCGTGAAATTCCT	1257
DB	1201	TCCACTATGCCCAATTTTGGTCAATCCCGCAAACTCTTTGTTCGAAGGGCGTGAAATTCCT	1260
QY	1258	TTGGTTAGCCAAAGAGAAAAACCATCGAGCTTGCAGCGGACGAGAAATGACCATCCGTGCT	1317
DB	1261	TTGGTAAAACAAAGAACAAACCATCGATCTTTCGACGGCAGAGAAATGACCATCCGTGCT	1320
QY	1318	TGTTGCGATTTTCTGACCTATGTGAAACTCGGACGGATAAAAACCGACCCGCCCGCTC	1377
DB	1321	TGTTGCGATTTTCTGACCTATGTGAAACTCGGACGGATAAAAACCGACCCGCCCGCTC	1380
QY	1378	AAACCGAAGCGGCAGATCAAGAGATTCGGACATTTGATATGCGGAGAAAGAGCAAGAC	1437
DB	1381	CAACCCGAAGCGGCAGATCAAGAGGGGACGAGAGGGGTGTAGGCGTTGATAACGGTAAA	1440
QY	1438	GAAATTTCCGAAGATGATAAACCGCGAAGATGAAGTCCACCGAAGAGAGAGGAGCTCAAGAA	1497
DB	1441	GAAA---GGGAAGACGAATTCGGCGATGAAGAAAGCCCGGAGA-----	1481
QY	1498	ACCGAAGAAAGAACTGATGAAGACGAAGAGGAAGAACCCGAAGAACTGAAGAAACTGAA	1557
DB	1482	--CGAAGTCGTAGAAGATGAAGACCGAAGATGAAGACGAGAGAGAAATCGAA-----GAA	1533
QY	1558	GAAACTGAAGAACTGAAGAAACTGAAGAACTGAAGAAAAATCGCCGACAGAAAGAGGC	1617
DB	1534	GAACCTGAGAGAAAGCTGAAGAGGAGAAACCCGAAGAGAAATTCGCGCAGAGAGAGGC	1593
QY	1618	AACGCGGTTTACGGCAGCATCTCGCCACTCGGAGCTCTAAAGCAGAGGACATCGAC	1677
DB	1594	AACGCGGTTTACGGCAGCATCTCGCCACTCGGAGCTCTAAAGCAGAGGACATCGAC	1653

1678	QY	CTTTTCTGAAAGGTATPCGCACGGCGGAAGCGGACATTCGCCAAATTTGGAAAGCAGCG	1737
1654	Db	CTTTTCTGAAAGGTATPCGCACGGCGGAAGCGGACATTCAAAAAACGGAACGGCGCAT	1713
1738	QY	TATACGGGCACTTGGGAAGCGCGTATCGCGGTCGCCGATAAAGAAAGCGCAACAGCTAGAT	1797
1714	Db	TATACGGGCACTTGGGAAGCGCGTATCGCGGTCGCCGATAAAGAAAGCGCAACAGCTAGAT	1753
1798	QY	GGCCTACGTCCATTCAAAAAGGATAGCTATGCGAATCAAGCGGCGAAAAAGCAGAAATTTGAC	1857
1754	Db	-GTGGTACGTCCATTCAAAAAGGATAGCTATGCGAATCAAGCGGCGAAAAAGCAGAAATTTACC	1812
1858	QY	GTTGATTTTGGTGGCGAAGTCGCTTTTCAGGTAAAGTTGACAGAAAAAATGATACACACCCC	1917
1813	Db	GTTGATTTTCGAAGCGCAAGACGGTCTCCGGAATGCTGACAGAAAAAATGATACAAACCCC	1872
1918	QY	GCTTTTATATATGAAAAAGGTGTGANTGATGGGCAACCGGTTTCCACGTTTGGCGCGTACT	1977
1873	Db	GCITTTTATATATGAAAAAGGTGTGANTGACGGTAAACGGTTTCCACGCTTTGGCGCGTACT	1932
1978	QY	CGTCAAAATCGTGTTGATTTGTCTGGCGCAAGTTTCGACTAATCCCAAAAGTTTAAAGCC	2037
1933	Db	CGGAGAAACGGTATATGACCTTTCGCGCAGGGTTCGACTAACCCGAAGAATTCAAAGCC	1992
2038	QY	AGTAATCTTCTCTGTAAGGAGGATTTATGGTCCGACGGCGGACAGTTGGGTGGTGAAT	2097
1993	Db	GACAATCTTCTTGTAAACAGGCGGCTTTTATGGCCGCGAGCGGCGAGAAATTTGGGCGGTAAAT	2052
2098	QY	ATTATCGACAGTGACCGGAAATTCGGCGTGCTATTCGGTGCAGAAAGATATCGACGAG	2157
2053	Db	ATTATCGACAGCGAGCCGGAATTTGGTGGCGGTATTTGGGCGCAAAAAAGATGCAACGAG	2112
2158	QY	GTGAAAAAATGA	2169
2113	Db	GCAACACGATGA	2124

### RESULT 3

US-10-282-122A-29815  
Sequence 29815, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931





Db	301	TTTAAAGAAAGGTGATGTTCTGTTTTTATACGGTTCAAAAAAGATATAAATCTTCAGTGGCTT	360
QY	355	AAAAGCGAAATTCATAACGTAATCCTTGAGGCAAGCAATTCACCATCGGAAATGAAAT	414
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QY	415	AAAAAATAATATATCGGTTTGTGTCAGTCCGGTTATGTTTATCTAATAAACCGAAAGAT	474
Db	421	AAAAAATAATGTTATGAAATTTGTGGATCCGGTTATGTTATATATCTTAAATAACCGAACAGAT	480
QY	475	GAAATTCGAAACATCGGATGAAAGCAGTTTCTAATCGTTAGGCTATGACGGTTT	534
Db	481	GAAATTCGAGTGCATTCGAAATCGCAAGCAGTTTCTAATCGTTTGGCTACGACGGTTT	540
QY	535	GTATATATCTCGGAGAACATCCTTCCCAATCTTTACCGAGCGCGGAAACGGTGAATAT	594
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QY	595	TCCGGCAATCGCAATATATGACCGATGCCATACGTATCGGAGAGTAA---GGGGTT	651
Db	601	TCCGGTAACTGGCAATATATGACCGATGCCATACGTATCGGAGAGTAAACGAGAGAT	660
QY	652	TCCAGTGTGATTTGCGTTTATACCAATATATGTTAATGTAATGAAATTTGGGCGACTTCTTAT	711
Db	661	CTAGCGAAGATTTGGGTTATCTCGTTTATAGGTCAAATGTCGAGCAATCTTAT	720
QY	712	GAGGCTAGGAGTSCCGATGCGCGGGAATAACATCTGCGCAATATACGTTAATTTGAC	771
Db	721	GCTGCGACTGCCGACGCGCGGAGGGAATAACATCTGCGCAATATACGTTAATTTGAT	780
QY	772	AAAAAAACCTGGAGTAAAGTTGATTAATAATCAGTATGTCGCAAGAGAGATGATCCT	831
Db	781	AAGAAACCTTCGACGGGTCAATTAATAATAATCAGTATGTCGCAAGAGAAACCGATGAA	840
QY	832	AAAAATCCACTGACCATTTCAACATTCGCAACATTCGAGCGCAACCGCTTTTACCGGC	891
Db	841	AAGAAACCTGACCATTTTACGACATTCGCAACATTCGAGCGCAACCGCTTTTACCGGC	900
QY	892	AGTGCCAAAGTTAGCACCGAGGTGAAGACGCAACACGCTGTATAAGAAATATTTGTTTTC	951
Db	901	AGTGCCAAAGTTTAAACCGAGTTGAAGACGAGCGCAACGCTGTATAAGAGCATTTGTTTTC	960
QY	952	CATACCGATGCCGATCAGCGGCTTGAGGGGTTTTTTCGGCATTAACGAGAGAGCTT	1011
Db	961	CATACCGATGCCGATCAGCGGCTTGAGGGGTTTTTTCGGCATTAAGGGGAGAGCTT	1020
QY	1012	GCGGGCGGTTTATCAGTAACGACAAACAGCGTATTCGGGCTGTTCGAGCAAAACAAA	1071
Db	1021	GCGGGAGGTTTATCAGTAACGACAAACAGCGTATTCGGGCTATTCGAGCA---AAAA	1077
QY	1072	ACAGAGACGACAAACGATCAGATACAAATCTCTGCGCTGCGCTCTGGAATAACACACAA	1131
Db	1078	ACAAACGATCAAAACGACGATACAAATCTCTGCTATGCGCTCTGGAATAACACACAA	1137
QY	1132	ATCTTGATTTCTTAAATTTCCGTTGACGAGCGACTGATGACCATGCCCTTAAGTTT	1191
Db	1138	ATCTTGATTTCTTAAATTTCCGTTGACGAGCGAGATTAATAATGCCCCCGCTT	1197
QY	1192	GCCATTTCCACTATGCCGATTTTGGTTCATCCGACAACTCTTGTGCAAGGCGGTGAA	1251
Db	1198	GCCATTTCCCTCTGCCGATTTTGGCATCCCGACAACTCTTGTGCAAGGCGGTGAA	1257
QY	1252	ATTCCTTTGTTAGCGAAGAAACCATGACGTTGCCGAGCGGCAAAATGACCATC	1311
Db	1258	ATTCCTTTGTTAGCGAAGAAACCATGACGTTGCCGAGCGGCAAAATGACCGTC	1317
QY	1312	CGTCTGTTGCGATTTTCTGACCTATGTAACCTCGGACGATTAATAACCGACCGCCC	1371
Db	1318	CGTCTGTTGCGATTTTCTGACCTATGTAACCTCGGACGATTAATAACCTGACCGCCA	1377
QY	1372	GCGGTCAAAACGAGGCGCAGGATGAAGAGATTCGGACATTTGATATGCGGAGAAAGC	1431
Db	1378	GCAAGTAAACCAAGGCGGAGATTAAGGAGGATGAAGAGGATACAGGCGTTGGTAAAC	1437
QY	1432	GAAGACGAATTTTCCGAGATGATAACGGCGAAGATGAAGTCAACGAAAGAGAGAGCT	1491
Db	1438	GACGAAGAGGCAACGGAAGATGAAGCCGACAGAGCGAGGAGGCGGAGACGAAATC	1497
QY	1492	GAAGAAACCGAAGAGAAACCTGATGAAGACGAGAGGAGAAACCGGAGAAACTGAGAA	1551
Db	1498	GGCGA---TGAAGGAGGAGGTGCGGAGAGACCGGAGAAACGAGAGGCGGCGAGAA	1554
QY	1552	ACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGCGACGAA	1611
Db	1555	-----GACGAGCTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGCGGCGACAA	1602
QY	1612	GAAGCAACGCGGTTTCAAGCAGCATCTGCGCACTCCGGAAGCCTCTTAAAGGCGAGGAC	1671
Db	1603	GGCGCGGTGTTGTTTCAAGCAGCATCTGCGCGCTCCGGAAGCTCTTAAGGCGAGGAT	1662
QY	1672	ATCGACCTTTTCTGAAAGGTATCGCACGGGGAAGCGGACATTCGCGCAATTTGGAATA	1731
Db	1663	ATCGACCTTTTCTGAAAGGTATCGCACGGGGAAGCGGACATTCGCGCAATTTGGAATA	1722
QY	1732	GACGCTATACCGGCACTTGGGAGCGGTATCGGCTGCGGATAAGAAAGCGGCAACAG	1791
Db	1723	GCACGCTATACCGGCACTTGGGAGCGGTATCGGCACTTCAATGGGACATCAT	1782
QY	1792	CTAGATGCGCACTACGTCATTCAMAAGGATAGCTATGCGAATCAAGCGGCAAAAGCAGAA	1851
Db	1783	GGCGAT-----AAAAAGCGGCAAAAGCAGAA	1809
QY	1852	TTTGAAGTTGATTTTGGTGGAGGTCGCTTTCAGTAAGTTGACAGAAATAATGATACA	1911
Db	1810	TTTGAAGTTGATTTTGGGCGAGAAATCGATTTTCGGAACGCTGACGAGAAACCGGTGTA	1869
QY	1912	CACCGCGCTTTTATATGAAAGGTGATGATGCAACGCTTCCACGCTTTGGCG	1971
Db	1870	CAACTGCTTTTCCATTTGAAACCGCGGTGATGAGGCAATGTTTCCACGCGACGCG	1929
QY	1972	CGTACTCGTGAATAATGTTGATTTGCTGGGCAAGGTTTCGACTAATCCCCAAGTTTT	2031
Db	1930	CGCACTCGGATTAACGCGATCATCTTTCGGGAATGATTCGACTAATCTCCAGTTTTC	1989
QY	2032	AAAGCGAGTAATTTCTCTGTAAGAGAGATTTTATGTTCCGAGCGGCGAGTTGGGT	2091
Db	1990	AAAGCGAATAATCTTCTTGAACAGCGGCTTTTACGCGCCGCGAGGAAATTTGGGC	2049
QY	2092	GGTAAATTTATCGACAGTCACCGGAA 2118	
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RESULT 5			
US-10-735-098-1			
; Sequence 1, Application US/10735098			
; Publication No. US20040131634A1			
; GENERAL INFORMATION:			
; APPLICANT: Petersson-Fernholm, Annika Margareta			
; APPLICANT: Tomassen, Johannes Petrus Maria			
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein			
; FILE REFERENCE: B45106C1			
; CURRENT APPLICATION NUMBER: US/10735,098			
; CURRENT FILING DATE: 2003-12-12			
; PRIOR APPLICATION NUMBER: 09/485,760			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: PCT/EP98/05117			
; PRIOR FILING DATE: 1998-08-10			
; PRIOR APPLICATION NUMBER: GB 9717423.9			
; PRIOR FILING DATE: 1997-08-15			
; PRIOR APPLICATION NUMBER: GB 9805544.8			
; PRIOR FILING DATE: 1998-02-05			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 2277			

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/ TYPE: DNA
/ ORGANISM: Neisseria meningitidis strain BNCV
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (100)...(2274)
US-10-735-098-1

Query Match
Best Local Similarity 79.1%; Pred. No. 2.2e-307;
Matches 1675; Conservative 0; Mismatches 332; Indels 111; Gaps 6;

QY 1 ATGTGTAAACCGAATTATGCGCGCAFTGTCCTTGTTGCCCTTACTTTTGGCATCTTGCATC 60
Db |||
QY 100 ATGTGTAAACCGAATTATGCGCGCAFTGTCCTTGTTGCCCTTACTTTTGGCATCTTGCATC 159
Db |||
QY 61 GCGCGCAATTCGCGCGTGCAGCTGTGTGCAATCAAGCCGACCGCGTACCCCGTCACT 120
Db |||
QY 160 GCGCGCAATTCGCGCGTGCAGCTGTGTGCAATCAAGCCGACCGCGTACCCCGTCACT 219
Db |||
QY 121 TTCAAGTCTAAGGAGCTTCCCACTTCGCCCTCGCGGTCTTCGGTAGAAACCGAGCGG 180
Db |||
QY 220 TTCAAGTCTAAGGAGCTTCCCACTTCGCCCTCGCGGTCTTCGGTAGAAATCAAGCGG 279
Db |||
QY 181 GTCAACGACCGCGCGTGCAGCAATGCGGCTGTGAGACGGAATACTGCTTTTCAT 240
Db |||
QY 280 GTCAACGCGCGCGCGTGCAGCAATGCGGCTGTGAGACGCGGAATACTGCTTTTCAT 339
Db |||
QY 241 CGTGAAGATGCGCGCAATTCGCAATAGCAAAACGAGCAAGAAAGCTGTCGTTTAAA 300
Db |||
QY 340 CGTGAAGATGCGCGCAATTCGCAATAGCAAAACGAGCAAGAAAGCTGTCGTTTCAA 399
Db |||
QY 301 GAAGTGTATGTTCTGTTTATACGGTTTCAAAAGAAATAAAGTTCACCACTTAAAGC 360
Db |||
QY 400 GAAGTGTATGTTCTGTTTATACGGTTTCAAAAGAAATAAAGTTCACCACTTAAAGC 459
Db |||
QY 361 GAATTCATAAACGTAACTCTGAGCAAGCATTTACCATCGGAATAAGAAATAAAGAA 420
Db |||
QY 460 GAATTCATAAACGTAACTCTGAGTGAATAGGACATCAGAAAGAAATAAAGAA 519
Db |||
QY 421 TATTAATTCGGTTGTGTCAGTGCCTGTTATGTTTACTTAAAGACGGAAGATGAAAT 480
Db |||
QY 520 TATGAATATAAATTTGTAGATGCAAGTTTATGTAT---ATGTAAAGGAAAGATGAAAT 576
Db |||
QY 481 GAGAAACATCGGATGAAAGCAGTTTCTAATCGTTTGGCTATGACGGTTTGTATAT 540
Db |||
QY 577 AAGTGGACTTCAGATTACAGCAGTTTTCACCGCTTAGGTATGACGGTTTGTATAT 636
Db |||
QY 541 TATCTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGAAACGGTGAATAATTCGCGC 600
Db |||
QY 637 TATTCGCGAGAACGTCCTTCCCAATCTTTACCGAGTGGGGAACGGTGGATATTCCTGGT 696
Db |||
QY 601 AACTGGCAATATGACCGGATGCCATACGTCATCGGAGAGTAAAGGGGTTTCAGTGTG 660
Db |||
QY 697 AACTGGCAATATGACCGGATGCCAAGCGTCATCGAGCAGTAAGCGGTTGGCATTGAC 756
Db |||
QY 661 GATTTGGGTTTATACCAATATATGTAATGTAATTCGGAATATACGGTTTTCGACAAAAG 780
Db |||
QY 817 GATGTCGACGAAAGGGAAGAAACATCTGCTGAATATACGTAAGTTTCGTTACAAAGC 876
Db |||
QY 781 CTGGAAGTAAATGATTAATAATCAGTATGTGCAAGAGAGATGATCTTAAAGATCCA 840
Db |||
QY 877 CTGACGGCGAGCTGATTAATAAACCAATATGTCAACCCAGTCGAGAAGC---AAAAACG 933
Db |||
QY 841 CTGACCAATTTACCAACATTACCGCAACATTCGACGGCAACCGCTTTACCGCAGTGCAG 900
Db |||
QY 934 CTGACCAATTTACCAACATTACCGCAGTTTAAACGCGCAACCGCTTTTACCGCAGTGC 993
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QY 901 GTTAGCACCGAGGTGAAGACGCAACGCTGTATAAAGAAATATTTGTTTTCATACCGAT 960
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Db 994 GTCAATCTCTGATTTAGCGAAAAGCCATGCAATAGGAGCATTTGTTTTTCCATGCCAT 1053
QY 961 GCCGATCAGCGCTTGAGGCGGTTTTTTTCGGCGATAAACGAGAAAGCTTGCAGGCGG 1020
Db |||
QY 1054 GCCGATCAGCGCTTGAGGCGGTTTTTTTCGGCGATAAAGGGGGAAGAGCTTGCAGCG 1113
Db |||
QY 1021 TTTATCAGTAAACGACAAACAGCGTATTTCGGCGTGTTCGAGGCAACAAAAACAGAGACA 1080
Db |||
QY 1114 TTTATCAGCAACGACAAACAGCGTATTTCGGTGTATTCGAGGCAACAAAAATAGCC---- 1168
Db |||
QY 1081 GCAAAAGCATCAGATACAAATCCTGCCCTGCGCTTGGAAAAACACACCAAAATCTTGGAT 1140
Db |||
QY 1169 -----CCGTGCCGTCTGGAAAAACACACCAAAATCTTGGAT 1203
Db |||
QY 1141 TCTCTAAAAATTTCCGTTTGACGAGCGCACTGATGACCATGCCCGTAAGTTTGCATTTCC 1200
Db |||
QY 1204 TCTCTGAAAAATTTCCGTTTGATGAGGCAAGTGGTGAATAATCCCGACCGGTTTCCCATTTCT 1263
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QY 1201 ACTATGCCGATTTTGGTTCATCCCGACAAACCTTTCTGTGGAAGGCGTGAAATCTCTTTG 1260
Db |||
QY 1264 CCTATGCCGATTTTGGTTCATCCCGACAAACCTTTCTGTGGAAGGCAATGAATACTCTTTG 1323
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QY 1261 GTTAGCCCAAGAGAAAAACCATCGAGCTTGCGGACGGGAGAAAAATCACCATTCGCTGTGT 1320
Db |||
QY 1324 GTTAGCCCAAGAGAAAAACCATCGAGCTTGCGGACGGGAGAAAAATGACCGTCACTGTCTGT 1383
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QY 1321 TGCATTTTCTGACCTATGTGAAACTCGGACGGATTAATAACCGACCGCCCGCTGCAAA 1380
Db |||
QY 1384 TGCAGCTTTTGA CCTAATGTGAAACTCGGACGGATTAATAACCGACCGCCCGCCGCAAA 1443
Db |||
QY 1381 CCGAAGGCGCAGGATGAAGAGATTCGACATTTGATATGCGAAGAAAGCGAAGCAAGAA 1440
Db |||
QY 1444 CCGAAGGCGCAGGACGAGAGATTCGACATTTGATATGCGAAGAAAGCGAAGCAAGAA 1503
Db |||
QY 1441 ATTTCCGAGATGATACGGGCAAGATGAAGTCAACGGAAGAGGAAGCTGAAGAAACC 1500
Db |||
QY 1504 ATCGCGATGAGGAAGAGGACCGCAAGATGCAGCGCAGGAGATGAAGGACGCAAGAA 1563
Db |||
QY 1501 GAAGAAGAACTGATGAAGACGAGAGAGAAAGCCCGAAGAACTGAAGAACTGAAGAA 1560
Db |||
QY 1564 GACGAAGCCACAGAAACGAGACGCGGAAGAA----- 1596
Db |||
QY 1561 ACTGAAGAACTGAAGAACTGAAGAAACTGAAGAAACTCGCGCAGAGAAGAGCAAC 1620
Db |||
QY 1597 -----GACGAAGCTGAAGAACTGAAGAAAGTCTGCG---GCGAAGGCAAC 1641
Db |||
QY 1621 GCGGTTTCAGGCAGCATCTTCCCATCTCCGGAAGCTCTTAAAGCAGGACATCGACCTT 1680
Db |||
QY 1642 GGCAGTTTCAACACGCCATCTCTGCTGTCGGAAGCTCTTAAAGCAGGATATCGACCTT 1701
Db |||
QY 1681 TTCTGAAAGGTATTCGCGACGGGAGCGGATTCGCGATTAAGAAAGCGCAATTCGAAAGCAGCTAT 1740
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QY 1741 ACCGCACTTTGGAAGCGGCTATCGGCTGTCGCGATTAAGAAAGCGCAATTCGAGTAGTGC 1800
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QY 1762 ACCGCACTTTGGAAGCGGCTATTCGCAACACCCATTCATGGAAGCAATCATGCGGAT--- 1818
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QY 1801 ACTACGTTCATTCAAAAGGATAGTATGGAATCAAGCGGCAAAAAGCAGAAATTTGACGTT 1860
Db |||
QY 1819 -----AAAGAAGCGCAAAAAGCAGTATTTACGTT 1848
Db |||
QY 1861 GATTTTGTGCGAAGTCTTTCAGGTAAGTTTCAGCAAGAAATAATGATACACACCGGCT 1920
Db |||
QY 1849 GATTTGCGCAAGAAATCGATTTCCGGAACGCTGACGGAAGAAACCGGTGTAGAACCCTGCT 1908
Db |||
QY 1921 TTTTATTAATAAAGAGTGTGATGATGCAACCGGTTTCCAGCTTTGCGGCTACTCGT 1980
Db |||
QY 1909 TTTCCGTTATTAATAAAGAGTGTGATGAGGCAAGCGGTTTCCATGCGGACAGCGGCTCTCG 1968
Db |||
QY 1981 GAAATGCGTGTGATTTGCTGCGCAAGGTTTCGACTTAATCCCAAAGTTTAAAGCCAGT 2040
Db |||
QY 1969 GATGCGCATCGACCTTTCCGCGGAGGTTTCGACCAAAACCGCAGATCTTCAAAGCTAT 2028
Db |||
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Qy	2041	AATCTTCTCTGAGAGAGATTTATGTTCCGAGGGGCGAGAGTTGGGTGGTAATTT	2100
Db	2029	GATCTTCGTGTAGAGAGGATTTTACGGCCGAGGCGGAGGAAATTGGGCGGTATTATT	2088
Qy	2101	ATCGACAGTACCGGAAA	2118
Db	2089	TTCAATAATGATGGGAAA	2106
RESULT 6			
US-10-735-098-7			
; Sequence 7, Application US/10735098			
; Publication No. US20040131634A1			
; GENERAL INFORMATION:			
; APPLICANT: Pettersson-Fernholm, Annika Margareta			
; APPLICANT: Tomassen, Johannes Petrus Maria			
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein			
; FILE REFERENCE: B45106C1			
; CURRENT APPLICATION NUMBER: US/10/735,098			
; CURRENT FILING DATE: 2003-12-12			
; PRIOR APPLICATION NUMBER: 09/485,760			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: PCT/EP98/05117			
; PRIOR FILING DATE: 1998-08-10			
; PRIOR APPLICATION NUMBER: GB 9717423.9			
; PRIOR FILING DATE: 1997-08-15			
; PRIOR APPLICATION NUMBER: GB 9805544.8			
; PRIOR FILING DATE: 1998-02-05			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 7			
; LENGTH: 2262			
; TYPE: DNA			
; ORGANISM: Neisseria meningitidis strain M990			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)...(2259)			
US-10-735-098-7			
Query Match			
Best Local Similarity 57.7%; Score 1250.6; DB 17; Length 2262;			
Matches 1641; Conservative 0; Mismatches 429; Indels 63; Gaps 7;			
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Db	1	ATGTGTAAACCGAATATAGGGGCAATGCTGTGGCCCTTACTTTTAGCATCTTGATC	60
Qy	61	GGGGCAATTTCCGGCTGAGCTGTGTCGAATCAACCGGACCGC-----	108
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Qy	109	TACCCCGTCACTTTTCAAGTCTAAGGACGTTCCCACTTCGCCCTCCCGGGTCTTCGTA	168
Db	121	GATTCAAATCTTCAATCTCTGGGATAAGCCTGCTCCAGCTCTCCGAGCCTTCGTA	180
Qy	169	GAAACACGCGGTGTAACAGCCGCGCTGGTGGGCAATGCGCTGTGACACCGAAT	228
Db	181	GAAATCACGCGGTGTAAGCGGCGCGCTGGTGGGCAATGCGCTGCGCAAGCGGAAT	240
Qy	229	ACTGCTTTTCATCGTGAAGATGGCAGCGCAATTCGGATAGCAAAACAAGCAGAGAAAG	288
Db	241	ATCGCAACTTTTGATTAATATGTAATGAATTTCCCAATAGTAAGCAGCAGAGGATAT	300
Qy	289	CTGTCTGTTTAAAGAGGTGATGTTCTGTTTATACGGTTTCAAAAGAAATAACTTCAA	348
Db	301	CTGCCGTCTAAGAGAGGATATCTCTGTTTATAGCGGTACGCCGAAAGAACAGGCTGAC	360
Qy	349	CACCTTAAACCGAATTCATTAACGTAATCTTGAGCAGCAGCATTACCATCGGAAT	408
Db	361	AAACTTTAAAGAGAAATCAACGGACGGCATCTTAATGCAACCAATCTTACGTCGGATTA	420
Qy	409	GAAATAAAAAATATATATTCGGTTTGTGTCAGTCCCGTTTGTATGTTTACTTAAAAACGGA	468

Db	421	AAAGATGATCGTATCAATATAATAATATGTCGGGCGCGATATGTTTATACTAGATATGGA	480
Qy	469	AAAGATCAAAATGAGAAAACATCGGATGAAAAGCAGTTTCTAATCGTTTAGGCTATGAC	528
Db	481	ACAGATGAAATCGAACAGAACTCAGCGGTAAAGCGGTACCCACCGCTTAGTTAGAC	540
Qy	529	GGTTTTCTATATATCTCGGAGAACATCTTCCCAATCTTTTACCGAGCGGGAAACGGTG	588
Db	541	GGTTTTCTATATATCTCGGAGAACGTCCTTCCCAATCTTTTACCGAGTGGGAAACGGTG	600
Qy	589	AAATATTTCCGCAAACTGGCAATATATGACCGATGCCATACGTCTATCGAGAGGTAAAGGG	648
Db	601	GAATATTTCTGTAATGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTACAGCG	660
Qy	649	GTTCCTCAGTGTGGATTTGGTTATACCAATATATGTTAATGTAATGGAATGGGCGCACTTCT	708
Db	661	GTTCGCAATGCAATTTGGTTATATCAATTTTATGTAACGATGTTGGTGCACTTCT	720
Qy	709	TATGAGGTAGGATGCGGATGCGCGGCGGAAAAACATCTCGCAATATACGGTTAATTTTC	768
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Db	781	GATAACAAAACCATGATGGCAAGCTGATTTAAATCAGTATGTCGAAATATAAAAGAT	840
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Db	841	GAACCAAAAAACCGCTGACCATTTTACGACATCTGCAAAATTTGACGCGCAACCGCTTT	900
Qy	886	ACCGGCTGCGCAAAAGTTAGCACCGAGGTGAAGACGCAACACGCTGTATAAGAAATTTTG	945
Db	901	ACCGGCTGCGCAAGTCAATCTGATTTAGGAAAAACCTTGCCTGCTAATGAGCGTTTG	960
Qy	946	TTTTTCCATACCGATGCGGATCAGCGGCTTGAAGGCGGTTTTTTCGGCGATTAACGAGAA	1005
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Qy	1006	GAGCTTGGCGGCGGTTTTATCAGTAACGACACAGCGTATTCGGCGGTGTTCCGAGCAAA	1065
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Db	1198	AGTTTGGCAATTTCTCTATGCGGATTTTGGTTCATCCGCAAAAATCTTGTTCGAGGG	1257
Qy	1246	CGTGAATTTCTTGGTTAGCCAAAGAGAAACCATCGAGTTGCCGCGGAGGAAATG	1305
Db	1258	CGTGAATTTCTTGGTTAGCCAAAGAGAAACCATCGAGTTGCCGCGGAGGAAATG	1317
Qy	1306	ACCATCCGCTGTTGTTGCGATTTTCTGACTATGTAAGCTCGGAGCGGATTAACACCGAC	1365
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Qy	1366	CGCCCCCGCTCAAAACCGGAGCGGAGGATTAAGAGGATTCGACATTTGATTAATGCGAA	1425
Db	1378	CGCCCCCGCAATTAACCAAGGCGGAGATTAAGAGGAGGATTAAGAGGAGGATTAAGAGG	1437
Qy	1426	GAAAGCGAAGACGAAATTTCCGAAAGATGATAACGGCGAGATGAAAGTCAACGAGAGAG	1485
Db	1438	GATAACGACGAGAAA---CGAAGACGAAAGCGGTAGAACGAAAGCGGCGGAGAGAC	1494
Qy	1486	GAAAGTGAAGAAACCGGAGGAGAACTGATGAAGACGAAAGGAGGAGAAACCGGAGAACT	1545

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Db 1495 GAAACT-----TCCGAAGAGGATAATGGCGAAGACGAAGAACCAACCCGCCGAGAGAA 1548
QY 1546 GAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA 1605
Db 1549 ACCGAAGAAGTTGATGAAGCCGAAGAGAGGAGGAGTTGAAGAACCCGGAAGAAATCGCCG 1608
QY 1606 ACAGAAAGAGGCAACCGCGGTTTCAGGACGATCCTCCGACATCCCGACATCCCGAAGCCTTAAGGC 1665
Db 1609 ---GCAGAAAGCNAACCGCGGTTTCAGGACGATCCTCCGACATCCCGAAGCCTTAAGGC 1665
QY 1666 AGGACATCGACTTTCTCTGAAGGTATCCGACGCGGAGAGCCGACATCCGCAAAAT 1725
Db 1666 AGGACATCGACTTTCTCTGAAGGTATCCGACGCGGAGAGCCGACATCCGCAAAAT 1725
QY 1726 GGAAGACGCGTATACCGGCTTTGGGAGCGCGTATCCGCGTCCGCGATGAAGAGC 1785
Db 1726 GGAAGACGCGTATACCGGCTTTGGGAGCGCGTATCCGCGTCCGCGATGAAGAGC 1785
QY 1786 GAACAGCTAGATGGCACTACGTCCTATCAAAAGGATAGCTATCGAATCAAGCGCAAA 1845
Db 1786 AATCAGCGGATG-----AAAAAGCGCAAA 1812
QY 1846 GCAGAAATGAGCGTTGATTTGGTGGAGAGTCTTTCAGGTAGTTGACAGAAAAAT 1905
Db 1813 GCAGAAATGAGCGTTGATTTGGTGGAGAGTCTTTCAGGTAGTTGACAGAAAAAT 1872
QY 1906 GATACACACCGCGCTTTTATATTCGAAAGGTGATGATGGCAACGTTTCCACGCT 1965
Db 1873 GCGTAGAACCTGCTTTCATATGAAGACGCGCAAGATTTGATGGCAACGTTTCCACGCG 1932
QY 1966 TTGGCGCTACTCTGTAAGAAATGGTGTGATTTGCTGGGCAAGTTTCGACTAATCCCA 2025
Db 1933 ACAGCGCGACTCGGAGCGCGCATCACTTTCGGAATGTTTCACCGACCCCA 1992
QY 2026 AGTTTAAAGCAGTAATCTTCTCTAGAGAGGATTTATGTTCCGCGCGGCGAG 2085
Db 1993 ACATTCAGCTAGTAATCTTCTCTAGAGAGGATTTTACGCGCGCGCGGAA 2052
QY 2086 TTGGGTGTAATATTCAGCAGTCACCGGAA 2118
Db 2053 TTGGCGGTACTATTTTCAATAATGATGGGAA 2085
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## RESULT 7

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US-10-343-561-15
; Sequence 15, Application US/10343561
; Publication No. US20040126389A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Dalemans, Wilfrid
; APPLICANT: Denoel, Philippe
; APPLICANT: Dequesne, Guy
; APPLICANT: Feron, Christiane
; APPLICANT: Garcon, Nathalie
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Thiry, Georges
; APPLICANT: Thonnard, Joelle
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: Vaccines Comprising Outer Membrane
; TITLE OF INVENTION: Vesicles from Gram Negative Bacteria
; FILE REFERENCE: B45260
; CURRENT APPLICATION NUMBER: US/10/343.561
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/EP01/08857
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: EP 00956369.3
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: GB 0103170.7
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 15
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; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-561-15
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Query Match 20.2%; Score 439.2; DB 17; Length 1000;
Best Local Similarity 71.4%; Pred. No. 1.7e-96;
Matches 681; Conservative 0; Mismatches 203; Indels 70; Gaps 5;
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QY 1210 GATTTTGGTCATCCCGACAACTTCTTGTGCGAGGGCGTGAATTCCTTTGGTAGCCAA 1269
Db 1 GATTTTGGTCATCCCGACAACTTCTTGTGCGAGGGCGTGAATTCCTTTGGTAGCCAA 60
QY 1270 GAGAAAAACCATCGAGCTTGCACGCGCAGAAAAATGACCATCGCTGCTTGTTCGATTTT 1329
Db 61 GAGAAAAACCATCGAGCTTGCACGCGCAGAAAAATGACCATCGCTGCTTGTTCGAGCTTT 120
QY 1330 CTGACCTATGTGAATCTCGGACGGATAAAAAACCGACCGCCCGCTCAAAACCGAAGCG 1389
Db 121 TTGACCTATGTGAATCTCGGACGGATAAAAAACCGACCGCCCGCAAGTAACCAAAGCG 180
QY 1390 CAGGATTAAGAGGATTCGACATTTGATTAATGGCGAAGAAAGCGAAGACGAATTTCCGAA 1449
Db 181 GAAGATAAAGGGA-----GGATGAAGAGAGTGCAGGC 213
QY 1450 GATGATAACGCGAAGATGAAGTCAACGGAAGAGAGGAGCTGGAAGAAACCGAAGAGAA 1509
Db 214 GTTGTAACGTCGAAGAG-----GCCAAGCGGAGTTCGAAAGATGAAGCGGAGAA 267
QY 1510 ACTGATGAAGACGAAGAGAGAAACCCGAGAAACTGGAAGAACTGGAAGAACTGAAGAA 1569
Db 268 GCCGAAGAAATCGTCGAAGAAAGAAACCCGAGAAAGAGCTGAAGAGGAGAAAGCT---GAA 324
QY 1570 ACTGAAGAACTGGAAGAACTGGAAGAAATTCGCCGACAGAAAGAGGCAACGCGGTTCA 1629
Db 325 CCCAAGAGTTGAAGAAACCCGAGAAATTCGCCGACAGAAAGAGGCGGAGCGGTTCA 384
QY 1630 GGCAGCATCTGCCCATCTCCGGAAGCCCTTAAAGCAGGGACATCGACCTTTCTCTGAAA 1689
Db 385 AACGCCATCTGCTGCTCGGAAGCTTAAAGCAGGGACATCGACCTTTCTCTGAAA 444
QY 1690 GGTATCGCAGCGCGGAGCGGACATTCGCCCAATTTGGAAGAACGCTATACCGGCACT 1749
Db 445 GGTATCGCAGCGCGGAGCGGACATTCGAAGAACCCGGAAGACACATATACCGGCACT 504
QY 1750 TGGGAAGCGCTATCGCGTCCGCGATGAAGAAAGGCGAAGAGCTAGATGGCACTACGTCC 1809
Db 505 TGGGAAGCGCTATCGCGCACAACCCATTTCAATGGGACAATCAGGCGGAT-----552
QY 1810 ATCAAAAGGATAGCTATGCGAATCAAGCGGCAAAAGCAGAAATTTGACGTTGATTTGGT 1869
Db 553 -----AAAGAGCGGCAAAAGCAGAAATTTACGTTAATTTCCGC 591
QY 1870 GCGAAGTCGCTTTTCAGTAAAGTTGACAGAAAAAATGATACACACCCCGCTTTTATATT 1929
Db 592 GAGAAATCGAATTTCCGGAACGCTGACGAGAAAAACGGTGTACAACTCTCTTCTATATT 651
QY 1930 GAAAAAGGTGTGATGATGCAACGGTTTCCAGCTTTGGCGGTACTCGTGAAGATGGT 1989
Db 652 GAAAAAGGTGATGATGCAACGGTTTCCAGCTTTGGCGGTACTCGTGAAGATGGT 711
QY 1990 GTTGATTTGTCTGGGCAAGGTTCCGACTAATCCCAAGTTTAAAGCAGTAACTCTCTC 2049
Db 712 ATCAATCTTTCCGGAATGTTTCGACCAACCCAGAACCTTCCAGTAGTAGTCTTCGT 771
QY 2050 GTAGAGGAGGATTTTATGTTCCGAGCGGCGAGAGTTGGTGGTGAATATTATTCAGAGT 2109
Db 772 GTAGAGGAGGATTTTACGCGCGGCA--GCGAGGAATTTGGCGGTATTATTTCATTAAG 830
QY 2110 GACCGGAAATCGCGTGGTATTTCGGTGGGAAGAGATATGAGAGGTGAA 2163
Db 831 GATGGGAAATCTCTTGGTAACTGAGGTACTGAAAAATAAAGTTGAAGTTGAA 884
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RESULT 8  
US-10-087-192-463/c  
; Sequence 463, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 463  
; LENGTH: 31124  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) - (31124)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-087-192-463

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Best Local Similarity 64.4%; Pred. No. 3.3e-12;  
Matches 145; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
QY 1391 AGGATGAAGAGATTCCGGACATTGATATGGCGAAGAGACCGAAGCGAAGAAATTCGGAG 1450  
Db 18558 AAGAAG 18499  
QY 1451 ATGATAACGGCGAAGATGAAGTCACCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1510  
Db 18498 AAGAAG 18439  
QY 1511 CTGATGAAGACGAAG 1570  
Db 18438 AAGAAG 18379  
QY 1571 CTGAAGAACTGAAGAACTGAAGAAATTCGCCGACAGAGAG 1615  
Db 18378 AAGAAG 18334

RESULT 9  
US-10-027-632-269927/c  
; Sequence 269927, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-09-28  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 269927  
; LENGTH: 635  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-269927

; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 269927  
; LENGTH: 635  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-269927  
Query Match 4.4%; Score 95.2; DB 13; Length 635;  
Best Local Similarity 63.0%; Pred. No. 1e-12; Indels 0; Gaps 0;  
Matches 145; Conservative 1; Mismatches 84; Indels 0; Gaps 0;  
QY 1385 AGCGCAGGATGAAGAGGATTCCGACATTGATATGGCGAAGAGAAACCGAAGACGAATTT 1444  
Db 452 AAGAGGAG 393  
QY 1445 CCGAAGATGATAACGGCGAAGATGAAGTCACCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1504  
Db 392 GAGAAGGAG 333  
QY 1505 AAGAACTGATCAAGACGAG 1564  
Db 332 AAG 273  
QY 1565 AAGAACTGAGAGAACTGAAGAACTGAAGAAATTCGCCGACAGAGAA 1614  
Db 272 AAGAAG 223

RESULT 10  
US-10-027-632-269927/c  
; Sequence 269927, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 269927  
; LENGTH: 635  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-269927

Query Match 4.4%; Score 95.2; DB 16; Length 635;  
Best Local Similarity 63.0%; Pred. No. 1e-12;  
Matches 145; Conservative 1; Mismatches 84; Indels 0; Gaps 0;  
QY 1385 AGCGCAGGATGAAGAGGATTCCGACATTGATATGGCGAAGAGAAACCGAAGACGAATTT 1444  
Db 452 AAGAGGAG 393  
QY 1445 CCGAAGATGATAACGGCGAAGATGAAGTCACCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1504





FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Oligonucleotide  
US-10-101-487-73

Query Match 4.2%; Score 91.4; DB 14; Length 530;  
Best Local Similarity 61.6%; Pred. No. 8e-12; 91; Indels 0; Gaps 0;  
Matches 146; Conservative 0; Mismatches 91

QY 1379 AACCGAAGCGCAGGATGAAGAGGATTCGGACATTGATATGCGAAGAAACCGAAGACG 1438  
DB 523 AAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 464  
QY 1439 AAATTTCCGAGATGATACCGCGAAGATGAGTACCGAAGAGGAGGAGGAGGAGGAGG 1498  
DB 463 AAGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 404  
QY 1499 CCGAGGAAGAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1558  
DB 403 AAGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 344  
QY 1559 AAACCTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAG 1615  
DB 343 AAGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 287

RESULT 14  
US-10-101-487-106  
; Sequence 106, Application US/10101487  
; Publication No. US20020169125A1  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, DAVID W.  
; APPLICANT: BERGMAN, PHILIP A.  
; APPLICANT: LOFQUIST, ALAN  
; APPLICANT: PIETZ, GREGORY E.  
; APPLICANT: TOMPKINS, CHRISTOPHER K.  
; APPLICANT: WAGGONER JR., DAVID W.  
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 077319/0329  
; CURRENT APPLICATION NUMBER: US/10/101,487  
; CURRENT FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: 60/277,705  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 106  
; LENGTH: 554  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Oligonucleotide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(537)  
US-10-101-487-106

Query Match 4.2%; Score 91.4; DB 14; Length 554;  
Best Local Similarity 61.6%; Pred. No. 8.2e-12;  
Matches 146; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1379 AACCGAAGCGCAGGATGAAGAGGATTCGGACATTGATATGCGAAGAAACCGAAGACG 1438  
DB 20 AAGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 79  
QY 1439 AAATTTCCGAGATGATACCGCGAAGATGAGTACCGAAGAGGAGGAGGAGGAGGAGG 1498  
DB 80 AAGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 139  
QY 1499 CCGAAGGAAGAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1558  
DB 140 AAGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 199

QY 1559 AAACCTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAG 1615  
DB 200 AAGAGGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 256

RESULT 15  
US-09-864-761-2534/c  
; Sequence 2534, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aemica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 2534  
; LENGTH: 496  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC011416.1  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6  
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 35  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:53:30 ; Search time 8347.06 Seconds  
(without alignments)  
11538.757 Million cell updates/sec

Title: US-10-735-098-5

Perfect score: 2226

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_phi.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_srs.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_fod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2226	100.0	2226	1	AF123380	AF123380 Neisseria
2	2226	100.0	2226	6	A98972	A98972 Sequence 5
3	2226	100.0	2226	6	BD074757	BD074757 Neisseria
4	1774.8	79.7	326301	1	NMA622491	AL162757 Neisseria
5	1538.6	69.1	2519	1	AF072890	AF072890 Neisseria
6	1499.8	67.4	2124	1	AF123383	AF123383 Neisseria
7	1499.8	67.4	2124	6	A98976	A98976 Sequence 9
8	1499.8	67.4	2124	6	BD074759	BD074759 Neisseria
9	1490.2	66.9	2277	1	AF022781	AF022781 Neisseria
10	1490.2	66.9	2277	6	A98968	A98968 Sequence 1
11	1490.2	66.9	2277	6	BD074755	BD074755 Neisseria
12	1490.2	66.9	5691	1	AF049349	AF049349 Neisseria
13	1487	66.8	2537	1	AF031432	AF031432 Neisseria
14	1477.2	66.4	9955	1	AE002504	AE002504 Neisseria
15	1477.2	66.4	349980	6	AX044033	AX044033 Sequence
16	1442.2	64.8	2262	1	AF123381	AF123381 Neisseria
17	1442.2	64.8	2262	6	A98974	A98974 Sequence 7
18	1442.2	64.8	2262	6	BD074758	BD074758 Neisseria
19	1375.8	61.8	2169	1	AF123382	AF123382 Neisseria
20	1375.8	61.8	2169	6	A98970	A98970 Sequence 3
21	1375.8	61.8	2169	6	BD074756	BD074756 Neisseria
22	716	32.2	1000	6	AX081510	AX081510 Sequence
23	716	32.2	1000	6	AX374691	AX374691 Sequence
24	553	24.8	3398	1	NMLBPAG	X79838 N.meningiti
25	239.8	10.8	3300	1	NGU16260	U16260 Neisseria g
26	239.8	10.8	3300	6	AX685922	AX685922 Sequence
27	141.8	6.4	3171	1	NMTR0A	X69214 N.meningiti
28	100.4	4.5	75588	9	AL356742	AL356742 Human DNA
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31	97.6	4.4	221659	2	AC128582	AC128582 Rattus no
32	97.6	4.4	237440	2	AC136574	AC136574 Rattus no
33	97.6	4.4	263081	2	AC115498	AC115498 Rattus no
34	97	4.4	194006	10	AL732441	AL732441 Mouse DNA
35	97	4.4	219626	10	AC098719	AC098719 Mus muscu
36	96.2	4.3	189483	2	AC120267	AC120267 Rattus no
37	96.2	4.3	205161	2	AC115451	AC115451 Rattus no
38	96.2	4.3	210322	2	AC123582	AC123582 Mus muscu
39	96.2	4.3	247106	2	AC108255	AC108255 Rattus no
40	96.2	4.3	260973	2	AC119104	AC119104 Rattus no
41	96.2	4.3	269126	2	AC106218	AC106218 Rattus no
42	96	4.3	213609	10	AC127341	AC127341 Mus muscu
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44	95.6	4.3	94333	2	AC140495	AC140495 Rattus no
45	95.6	4.3	214976	2	AC114151	AC114151 Rattus no

# ALIGNMENTS

RESULT 1	AF123380	AF123380	2226 bp	DNA	linear	BCT 24-MAY-1999
LOCUS	Neisseria meningitidis strain H44/76	precursor (1bpB) gene, complete cds.				
DEFINITION	Neisseria meningitidis					
ACCESSION	AF123380					
VERSION	AF123380.1	GI:4084686				
KEYWORDS	Neisseria meningitidis					
SOURCE	Neisseria meningitidis					
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;					
REFERENCE	1 (bases 1 to 2226)					
AUTHORS	Patterson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tommassen,J.					

Thu Aug 26 10:18:15 2004

us-10-735-098-5.rge

Sequence variability of the meningococcal lactoferrin-binding

TITLE  
protein lbp  
JOURNAL  
Gene 231 (1-2), 105-110 (1999)  
MEDLINE  
99250255  
PUBMED  
10231574  
REFERENCE  
2 (bases 1 to 2226)  
AUTHORS  
Petersson, A., van der Biezen, J., Joosten, V., Heydriksen, J. and Tomassen, J.

TITLE  
Direct Submissi  
JOURNAL  
Submitted (26-JAN-1999) Department of Molecular Cell Biology,  
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands  
FEATURES  
Location/Qualifiers

1..2226  
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/mol\_type="genomic DNA"  
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DVTPPAKPSLETPVPSTGPAVGAAMRLRLRIATSKVGNDFPNQKAEKLSFK  
EGDLFLVGSQKDLKIHQNPVNEIRTSNENKYGVEFVDVGYVYTKNGTD  
ELWTSNRKQFSNRGDFVYVYSGEHSQSLPSAGTVQYSCNMVMDAIHRGTGA  
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GPDSLDGLVYVYVQNGVATSAATADDERGHPARYVDFPKKLTITGLQILNQVQK  
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ORIGIN

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## RESULT 2

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VERSION A98972.1 GI:6781932
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Neisseria meningitidis
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Neisseriaceae; Neisseria.
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Petersson-Fernholm, A.M. and Tommassen, J.P.
TITLE NISSERIA LAQTOFERRIN BINDING PROTEIN
JOURNAL Patent: WO 9909176-A 5 25-FEB-1999
UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIKA MAR (NL)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 2226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1441 GAAGAAAGCGCAGAGATGAAGCGCAGAGAGCGCAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
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Qy 1501 GATCAAGGAGGAGTGGCGAAGACGAAAGCGCAGAAACGAAAGCGGCGAAGAGACGAA 1560  
Db 1501 GATCAAGGAGGAGTGGCGAAGACGAAAGCGCAGAAACGAAAGCGGCGAAGAGACGAA 1560

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Qy 1681 GGTAATCCGCGAGCGGAGCGCATTTCCGCAAACTGCAAAAGCAGCTATACCGGCACT 1740  
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Qy 1741 TGGGAAGCGGTATCAGCAAAACCCATTCATTTGGCACAATCATGCGGATATAAAAAAGCGCA 1800  
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Qy 1861 AACGGTGTACAACTGCTTTCCATTTGAAAAAGCGCGTGAATGAGGCAATGTTTCCAC 1920  
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Qy 1921 GCGACAGCGGCACTCGGGATAACGGCATCAATCTTTCCGGGAAATGATTCGACTAATCCT 1980  
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Qy 1981 CCAAGTTTCAAGGCAATTAATCTTTGTAACAGGCGGCTTTTACCGCGCGCGAGCGGAG 2040  
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Qy 2041 GAAATGGGCGGTACTATTTTCAATTAATGATGGGAAATCTCTTGGTATTAATGAAAGTACT 2100  
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Qy 2101 GAAATGAAGCTGAAGCTGAAGTTGAAATGAAGCTGGTGTGGCGAAGCTTAAACCT 2160
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Db 2161 GAAGCTAAACCCCAATTCGGCGTGGTATTTCGGTGGCAAGAAGATAATAAAGAGGTGAA 2220
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Qy 2221 AAATGA 2226
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Db 2221 AAATGA 2226
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|
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RESULT 4
NWA622491/c
LOCUS Neisseria meningitidis serogroup A strain Z2491 complete genome;
DEFINITION segment 6/7.
ACCESSION AL162757 AL157959
VERSION AL162757.2 GI:7380371
KEYWORDS
SOURCE Neisseria meningitidis Z2491
ORGANISM Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 326301)
AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,
Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N.,
Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,
Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,
Skelton,J., Whitehead,S., Spratt,B.G. and Barrall,B.G.
TITLE Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491
JOURNAL Nature 404 (6777), 502-506 (2000)
MEDLINE 20222556
PUBMED 10761919
REFERENCE 2 (bases 1 to 326301)
AUTHORS Parkhill,J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT
Details of N. meningitidis sequencing at the Sanger Centre are
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
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434..453
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repeat_unit
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repeat_unit

misc_feature
misc_feature
gene
CDS

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desuccinylase, len: 381aa; similar to many eg. SW:P24176
(DAPE_BCOI) dapE, succinyl-diaminopimelate desuccinylase
from Escherichia coli (375 aa) fasta scores; E(): 0, 56.9%
identity in 371 aa overlap. Contains Pfam match to entry
PF01546 Peptidase_M20."
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252.50, E-value 5.7e-72"
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/note="Core DNA uptake sequence: gccgtctgaa"
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/note="NMA1731, conserved hypothetical protein, len:
206aa; similar to SW:P44013 (Y552_HAEIN) hypothetical
protein from Haemophilus influenzae (207 aa) fasta scores;
E(): 0, 59.6% identity in 203 aa overlap."
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/note="NMA1732, conserved hypothetical protein, len:
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E(): 0, 49.7% identity in 169 aa overlap."
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membrane protein from Neisseria meningitidis (183 aa)
fasta scores: E(): 0, 96.7% identity in 183 aa overlap.
Contains Pfam match to entry PF00127 copper-bind, Copper
binding proteins, plastocyanin/azurin family and prosite
match to PS00196 Type-1 copper (blue) proteins signature."
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binding proteins, plastocyanin/azurin family, score
218.60, E-value 9.1e-62"
/complement(3212..3259)
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/notes="PS00196 Type-1 copper (blue) proteins signature."
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len: 916aa; similar to many eg. SW:P10408 (SECA_ECOLI)
preprotein translocase SecA subunit from Escherichia coli
(901 aa) fasta scores: E(): 0, 58.0% identity in 920 aa
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99..79.7% Score 1774.8; DB 1; Length 326301;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 1990; Conservative 0; Mismatches 212; Indels 48; Gaps 4;

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Db |GCGCGCAATTTCCGCGTGCAGCTTGTTCGAATCAACGCGCGACCGGTAACCGCGTCACT 18922
QY 121 TTCAAGTCTAAGGACGCTTCCCACTCCGCCCCCTTCCCAACCTTCTATAGAAACCAACGCCG 180
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QY 181 GTGCCGTC AACCGCGCTCCCGTCCGTCGCGCAATGCGGCTGTTCAGGGCGGATTTTCGCA 240
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QY 961 CATACCGATCCGATCAGCGCTTTGAGGGCGGTTTTTTTCGCGATAGAGGGGAGAGAGCTT 1020
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QY 1021 GCCCGAGCTTTATCAGCAACAGCAACAGCTATTTCCGCGTATTCGAGGCA---AAAAA 1077
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QY      2218 GAAAAATGA 2226
Db      2488 GAAAAATGA 2496

RESULT 6
AF123383
LOCUS
DEFINITION
Neisseria meningitidis strain 881607 lactoferrin-binding protein
precursor (lbpB) gene, complete cds.
ACCESSION
AF123383
VERSION
AF123383.1 GI:4884692
KEYWORDS
Neisseria meningitidis
SOURCE
Neisseria meningitidis
ORGANISM
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 2124)
Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and
Tomassen,J.
TITLE
Sequence variability of the meningococcal lactoferrin-binding
protein lbpB
JOURNAL
Gene 231 (1-2), 105-110 (1999)
MEDLINE
99250255
PUBMED
10231574
REFERENCE
2 (bases 1 to 2124)
Pettersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and
Tomassen,J.
TITLE
Direct Submission
JOURNAL
Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
LOCATION/Qualifiers
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## ORIGIN

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Query Match      67.4%; Score 1499.8; DB 1; Length 2124;
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Matches 1779; Conservative 0; Mismatches 317; Indels 39; Gaps 5;

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QY      361 AAGAGTAAATTCATCAACGCAATCTAATGATGAGAAATAGGACATCAGAAATGAAAT 420
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QY      421 AAAAAATATGTTATCAATTTCTGATGCGGTTATGATATATATACTAAAAACGGAACAGAT 480
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QY      481 GAAATGTAGTGACATTCRAATCGCAAGCATTTTCTAATCGTTTGGCTACGACGGTTTT 540
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QY      541 GTATATATTTCGGAGAACATCTTTCCCAATCTTTTACCGAGCGCGGAGCGTGAATAT 600
Db      535 GTATATATTTCGGAGAACATCTTTCCCAATCTTTTACCGAGCGCGGAGCGTGAATAT 594
QY      601 TCCGTAATCTGGCAATATATGACCGATGCCATACGTCTCGAACAGGAAAGCAGAGAT 660
Db      595 TCCGCAACTGGCAATATATGACCGATGCCATACGTCTCGAACAGGAAAGCAGAGAT 654
QY      661 CTTAGCGAAGATTTGGGTTATCTCGTTTATACGCTCAAAATGTGCGAGCACTTCTTAT 720
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Db      895 AGTGCAAAAGTTAAACACAGAGGTGAAGAGCAATCAGCTGATTAAGAGATATTTGTTTTTC 954
QY      961 CATACCGATGCGGATCAGCGGCTTGAGGCGGTTTTTTCGCGGATTAAGGGGAAAGAGCTT 1020
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QY 901 AGTGGCAAAAGTTTAAACACCGAGTTTGAAGACGAGCAGCTGTATGAAGAGAGATTTGTTTTC 960  
DB 902 AGTGGCAAAAGTTTAAACACCGAGTTTGAAGACGAGCAGCTGTATGAAGAGAGATTTGTTTTC 960  
QY 895 AGTGGCAAAAGTTTAAACACCGAGTTTGAAGACGAGCAGCTGTATGAAGAGATTTGTTTTC 954  
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## RESULT 8

BD074759 2124 bp DNA linear PAT 27-AUG-2002  
LOCUS Neisseria lactoferrin-binding protein.  
DEFINITION  
ACCESSION BD074759  
VERSION BD074759.1 GI:22620362  
KEYWORDS JP 2001514894-A/5.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 2124)  
AUTHORS Fellholm, A.M.P. and Thomassen, J.P.M.  
TITLE Neisseria lactoferrin-binding protein  
JOURNAL Patent: JP 2001514894-A 5 18-SEP-2001;  
UNIVERSITY OF UTRICHT, TECHNOLOGY FOUNDATION  
COMMENT OS Unidentified  
PN JP 2001514894-A/5  
PD 18-SEP-2001  
PF 10-AUG-1998 JP 2000509840  
PR 15-AUG-1997 GB 9717423.9, 05-FEB-1998 GB 9802544.8 PI  
ANICA MARGARETA PETERSON FELLHOLM, JOHANES PETRUS MARIA PI

THOMASEN	
PC	C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22, C07K16/12, C12N1/02, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC
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CC	Strandedness: Double;
CC	Topology: Linear;
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Best Local Similarity 83.3%; Pred. No. 1.7e-294;	
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Qy	61 GGCGCAATTTCCGGCTGACGCTGTGTGTCGAATCAACCGCGACCGGTACCCGTCAC 120
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Qy	121 TTCAAGTCTAAGGACGTTTCCCACTCCGCGCTGCGCAATGCGGCTTATAGAAACACGCG 180
Db	121 TTCAAGTCTAAGGACGTTTCCCACTCCGCGCTGCGCAATGCGGCTTATAGAAACACGCG 180
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Db	235 ACTTCTGATAGGTGGCAATGATTTCCAAATAGCAAAACAGCAGAAAGAACTGTG 294
Qy	301 TTTAAGAAAGGTGATGTTCTGTTTATAGGTTTCAAAAGAAAGATTAACGTCGTT 360
Db	295 TTTAAGAAAGGATATCTGTTTATAGGTTTCAAAAGAAAGATTAACGTCGTCAGCTT 354
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Db	355 AAGGATAAATTCATCAACGCAATCTTAAATGTAGAAATAGGACATCAGAAATGAAAT 414
Qy	421 AAAAAATATGTTATGAAATTTGGATGCGGTTATGATATATATATATATATATATAT 480
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Db	1315 CGTCTTGTGTGCGATTTTCTGACCTATGTGAAATCTCGGACGCGATAAAAATGACCGCCA 1374
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Db					
QY	1021	GCCGGA	CGGTTTTATCAGCAACGACAAACGCGTATTCGCGGTATTCGAGCGCAAAACCA	1080	
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QY	1105	GCCGGA	CGGTTTTATCAGCAACGACAAACGCGTATTCGCGGTATTCGAGCGCAAAAC	1160	
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Db					
QY	1161	-----	-----	AAATAGCCCGTGCCTCTGGAACACACCAAAATC	1197
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QY	1603	GCTGA	GAACCT-----	GAAGAGAAATCCTCGGCGAGAGGCAC---	1650
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Db					

[illegible]



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1543	GAGATGAGGAGCGAAGAGACGAGGCCACAGAAACGAGACGCGCGAGAGACGAA	1602
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1981	CGAAGTTTCAAGCCCAATATCTTCTGTTGTAACAGGCGGCTTTTACGCGCGCAGGCGGAG	2040
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LOCUS BD074755 2277 bp DNA linear PAT 27-AUG-2002  
DEFINITION Neisseria lactoferrin-binding protein.  
ACCESSION BD074755  
VERSION BD074755.1 GI:22620358  
KEYWORDS JP 2001514894-A/1.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
1 (bases 1 to 2277)  
REFERENCE Felnholm, A.M.P. and Thomsen, J.P.M.  
AUTHORS Neisseria lactoferrin-binding protein  
TITLE Patent: JP 2001514894-A 1 18-SEP-2001;  
JOURNAL UNIVERSITY OF UTRICHT, TECHNOLOGY FOUNDATION  
COMMENT OS Unidentified  
PN JP 2001514894-A/1  
PD 18-SEP-2001  
PF 10-AUG-1998 JP 2000509840  
PR 15-AUG-1997 GB 9717423.9, 05-FEB-1998 GB 9802544.8 PI  
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C07K16/12,  
PC C12N1/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC  
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CC Topology: Linear;  
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Query Match 66.9%; Score 1490.2; DB 6; Length 2277;  
Best Local Similarity 82.7%; Pred. No. 1.6e-292;  
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QY 61 GCGGCAATTTTCGGCGTCAGCCTGTTCTGCAATCAACGCGACCGCGTACCCGTCAT 120  
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QY 421 AAAAAATATGTTATGAATTTGTGATGCGCGTTATGTATATATACTAAAAACGGAACAGAT 480  
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Db	2071	GAATTTGGCGGTACTATTTTCAATATGATGGAATCTCTTGGTATACTGAAATACT	2130
Qy	2101	GAAATGAAGCTGAAGCTGAAGTTGAAATGAAGCTGGTGT-----	2141
Db	2131	GAAATGAAGCTGAAGCTGAAGTTGATTTGATTTGATTTGATTTGATTTGATTTGAT	2190
Qy	2142	--TGGCGACAGTTAAACCTGAGCTAAACCCCAATTCGGCTGCTATTTCGTTGCGAAG	2199
Db	2191	GATGTTGAACAGTTAAACCTGAGCTAAACCCCAATTCGGCTGCTATTTCGTTGCGAAG	2250
Qy	2200	AAAGATAATAAGAGGCTGGAATAATGA	2226
Db	2251	AAAGATAATAAGAGGCTGGAATAATGA	2277
RESULT 12			
AF049349		5691 bp	DNA linear
LOCUS			
DEFINITION			Neisseria meningitidis lactoferrin binding protein B precursor (lbpB) and lactoferrin binding protein A precursor (lbpA) genes, complete cds.
ACCESSION			AF049349
VERSION			AF049349.1
KEYWORDS			GI:3582727
SOURCE			Neisseria meningitidis
ORGANISM			Neisseria meningitidis
REFERENCE			Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
AUTHORS			1 (bases 1 to 5691)
TITLE			Lewis, L.A., Rohde, K., Gipson, M., Behrens, B., Gray, E., Toth, S.I., Roe, B.A., and Dyer, D.W.
JOURNAL			Identification and molecular analysis of lbpB, which encodes the two-component meningococcal lactoferrin receptor
MEDLINE			Infect. Immun. 66 (6), 3017-3023 (1998)
PUBMED			9596785

REFERENCE	2 (bases 1 to 5691)
AUTHORS	Lewis, L.A., Rohde, K., Gipson, M., Behrens, B., Gray, E., Toth, S.I., Roe, B.A., and Dyer, D.W.
TITLE	Direct Submission
JOURNAL	Submitted (19-FEB-1998) Microbiology and Immunology, University of Oklahoma Health Sciences Center, 1035 EWSB / 940 SL Young Blvd., Oklahoma City, OK 73104, USA
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KEYWORDS  
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Neisseria meningitidis MC58  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
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AUTHORS		Pizza, M.; Hickey, E.; Peterson, J.; Tettelin, H.; Venter, J. C.;	
		Marignani, V.; Galeotti, C.; Mora, M.; Ratti, G.; Scariselli, N.;	
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Qy	595	CAATATTCGGTAACTGGCAATATATGACCGATGCGCATGCTCATCGAACGGAAGAAACGA	654
Db	98887	CAATATTCGGTAACTGGCAATATATGACCGATGCGCATGCTCATCGAACGGAAGAAACGA	98829
Qy	655	GGAGATCTTAGCGAAGATTTGGGTTATCTCGTTTATTTACGGTCAAAAATGTCGGAACAAT	714
Db	98828	--GGTTCCAGTACGATTTGGGTTATCCCATATTTATGTTATGAAATTTGGGCAACT	98771
Qy	715	TCTTATGCTGCGACTGCGCAGCAGCCGGGAGGAAACATCTCTCCGCAATATACGTTGAT	774
Db	98770	TCTTATGAGGCTAGGATGCGCAGCAGCAGGAAAGCATCTCTCCGCAATATACGTTGAT	98711
Qy	775	TTGATAAGAAACTTTTGAACGGGTCAATTAATTTAAATCTAGTATGTGCAAAAGAAACCC	834
Db	98710	TTTGATAACAAACCCCTGAATGGCAAGCTGATTTAAATATCAGTATGTGCAAAATAAAAGT	98651
Qy	835	GATGAA-----AAGAAACCACTGACCATTTACGACATTTACCGCAACATTTGACCGC	885
Db	98650	AATCCAAATGAGCCCAAAAAACCGCTGACCATTTTACGACATTTACCGCAACATTTGACCGC	98591
Qy	886	AACCGCTTTACCGCAGTGCCTAAAGTTTAAACCGGAGTAAAGACGAGCAGCAGCTGATAAA	945
Db	98590	AACCGCTTTACCGCAGTGCCTAAAGTTTAAACCGGAGTAAAGACGAGCAGCAGCTGATAAA	98531
Qy	946	GAGCATTTGTTTTTCCATACCGATGCGGATGCGGCTTGAAGGCGGTTTTTTCGGCGAT	1005
Db	98530	GAAATATTTGTTTTTCCATACCGATGCGGATGCGGCTTGAAGGCGGTTTTTTCGGCGAT	98471
Qy	1006	RAGGGGAGAGCTTTCGGCGGTTTATTCAGCAACGACACACAGCGTATTCGGCGTATTC	1065
Db	98470	AACGAGAAGAGCTTTCGGCGGTTTATTCAGCAACGACACACAGCGTATTCGGCGTATTC	98411
Qy	1066	GCAGGCA---AAAAACAAACGCAATCAACCGCAGCAGATACAAATCTTCTATGCGGTCT	1122
Db	98410	GCAGGCAACAAACAAACGAGACAGAAAAACCGCAGCAGATACAAACCTGCCCTGCTCT	98351
Qy	1123	GAAAAACACCAAAATCTTGGATTTCTTGAAAAATTTCCGTTGACGAGCGGAGGATAA	1182

Search completed: August 24, 2004, 23:47:28  
Job time : 8363.06 secs

Db 98350 GGAAAAACACACCAAAATCTTGGATCTCTGAAAAATTTCCGTTGACGAGCAAGTGATAAA 98291  
QY 1183 AATGCCCGCCGCTTTCSCCATTTCCCTCTGCCCGATTTTGGCCATCCCGACAAATCTCCTT 1242  
Db 98290 AATCCCGTGAGTTTCCCATTTCTCTATGCCCGATTTTGGTTCATCCGACAAATCTCTT 98231  
QY 1243 GTCGAAGGCGTGAAATCTCTTTGGTTAGCAAGAGAAACCAATCGAGCTTCCGACGGC 1302  
Db 98230 GTCGAAGGCGTGAAATCTCTTTGGTTAAACAAGAACAACCAATCGAGCTTCCGATGGT 98171  
QY 1303 AGGAAATACCGTCCGCTCTGTTGCGATTTTCTGACCTATGTGAAATCGGACGGATA 1362  
Db 98170 AGGAAACGCAATCGAACCTCTCGGATTTTCTGACCTATGTGAAATCGGACGGATG 98111  
QY 1363 AAAAAGTACCGCCAGCAAGTAACCAAGGCGGAAGATAAGGGAAGGATGAAGAGAT 1422  
Db 98110 CAAACCGAACGTCCTCCGCCCAACCGAAGGCGGAGGAGGAGGAGGAGGAGGAT 98051  
QY 1423 ACAGCGTTGTGTAACGAGCAAGGACGGAAGATGAAGCCGACAGAGGCGGAGGAGGA 1482  
Db 98050 ACAGCGTTGTATAGCGTGAAGAGGCGGAAGACGAAATCGACGATGAA -----GAAGGC 97997  
QY 1483 GCGGAAGACGGAATCGGCGATGAAGGAGAGGTGCGGAAGACGAAGCCGCAAGAAACGAA 1542  
Db 97996 ACCGAAGACGCGCGCTAAAGACGAAGGACGAGGAGGAGGAGGAGGAGGAGGAGG 97937  
QY 1543 GCGGCGGAAGAGACGAGCTGAAGAACCTGAAGAACCCGAGAGAGAGATCCGCGCAGAA 1602  
Db 97936 -----GATGAAGCTGAAGAACCCGAGAGAGAAATCGCCGACAGAA 97898  
QY 1603 GCGGCGGTGTGTGTTACAGCGGATCTCTGCCGCTCCGGAAGCTCTTAAAGGCGAGGAT 1662  
Db 97897 GAAGCGGCGAGCGGTTACAGCGGATCTCTGCCGCTCCGGAAGCCCTTAAAGGCGAGAAC 97838  
QY 1663 ATCGACCTTTTCTGAAAGGTATCGGACGCGGGAAGCCGACATTCGCAAACTGGAAA 1722  
Db 97837 ATCGACCTTTTCTGAAAGGTATCGGACGCGGGAAGCCGATATTCGAAACTGGAGAA 97778  
QY 1723 GCACGTATACCGGCACCTTGGGAAGCGGTATCAGCAACCCATTCATGGGACAAATCAT 1782  
Db 97777 GCACGTATACCGGCACCTTGGGAAGCGGTATCAGCAACCCATTCATGGGACAAATCAT 97718  
QY 1783 CCGGNTAAAGCGGCAAGAGAAATTTGACGTTGATTTCCGCGAGAGAAATCGATTCC 1842  
Db 97717 CCGGNTAAAGCGGCAAGAGAGATTTACCGTTGATTTCCGCAAGAAATCGATTCC 97658  
QY 1843 GGAACGCTGACGGAAGAAACGGTGTACACCTCTTCCATATTTGAAAAACGCGTGAT 1902  
Db 97657 GGAACGCTGACGGAAGAAACGGTGTAGAACCTCTTCCATATTTGAAAAACGCGCAAGAT 97598  
QY 1903 GAGGCAATGTTTCCACGCGCAGACGCGCAGCTCGGATTAACGCGCATCATCTTTCGGGA 1962  
Db 97597 GAGGCAATGTTTCTACGCGCAGACGCGCAGCTCGGATTAACGCGCATCATCTTTCGGGA 97538  
QY 1963 ATGATTCGACTAATCTCTCAAGTTTCAAAGCCAAATCTTCTTGTAAACAGCGGCTTT 2022  
Db 97537 ATGATTCGACTAATCTCTCAAGTTTCAAAGCTAGTAATCTTCTGTAGAGGCGGATTT 97478  
QY 2023 TACGCGCGCAGCGGAGGAAATTTGGCGGTACTATTTTCAATATGATGGGAAATCTCTT 2082  
Db 97477 TACGCGCGCAGCGGAGGAAATTTGGCGGTATTTATTTTCAATATGATGGGAAATCTCTT 97418  
QY 2083 GGTATAACTGAAGATACTGAAAA-----TGAAGCTGAAGCTGAAGTTGAAATGAAGCT 2136  
Db 97417 GGTATAACTGAAGATACTGAAAAATGAAGTTGATTTGAAGCTGAAGTTGATGCTGAAGTT 97358  
QY 2137 GGTGTTGGCGAACAGTTTAAACCTGAAGCTTAAACCCCAATTCGCGGTGATTTCCGTCG 2196  
Db 97357 GATGTTGGCAACAGTTTAGAATCTGAAGTTAAACCAATTCGCGGTGATTTCCGTCG 97298  
QY 2197 AAGAAAGATAATGAAGAGTGGAAAAATGA 2226  
Db 97297 AAGAAAGATAATGAAGAGTGGAAAAATGA 97268



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:48:44 ; Search time 754.168 Seconds  
(without alignments)  
12538.967 Million cell updates/sec

Title: US-10-735-098-5  
Perfect score: 2226  
Sequence: 1 atgtgtaaacccgaattatgg.....ataaagaggtggaataatga 2226

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2226	100.0	2226	2	AAX23321	Aax23321 N. mening
2	1774.8	79.7	2226	7	ACA41945	Aca41945 Prokaryot
3	1499.8	67.4	2124	2	AAX23323	Aax23323 N. mening
4	1490.2	66.9	2277	2	AAX23319	Aax23319 N. mening
C 5	1477.2	66.4	110000	3	AAX23319	Continuation (2 of
C 6	1477.2	66.4	349980	3	AAX21611	Aaf21611 Neisseria
7	1442.2	64.8	2262	2	AAX23322	Aax23322 N. mening
8	1375.8	61.8	2169	2	AAX23320	Aax23320 N. mening
C 9	1077.6	48.4	14652	3	AAA81482	Aaf91389 N. mening
10	716	32.2	1000	4	AAE91389	Abk37769 DNA sequ
11	716	32.2	1000	6	ABK37769	Aaa81815 N. mening
12	390.4	17.5	707	3	AAA81815	Abb67377 Neisseria
13	239.8	10.8	3300	6	ABK67377	Aas90909 DNA encod
14	91.2	4.1	379	5	AAS90909	Aas75428 DNA encod
15	91.2	4.1	379	5	AAS75428	Ade09716 Novel DNA
16	91.2	4.1	379	9	ADR09716	Aas90688 DNA encod
17	90.2	4.1	621	5	AAS90688	Aas75460 DNA encod
18	89.8	4.0	400	5	AAS75460	Aas68580 DNA encod
19	89.8	4.0	963	5	AAS68580	Aas92079 DNA encod
C 20	87	3.9	453	5	AAS92079	Aas90738 DNA encod
21	87	3.9	1072	5	AAS90738	Aaz23896 Murine LO
22	87	3.9	49999	2	AAZ23896	Aax23891 Murine LO
23	87	3.9	49999	2	AAZ23891	

24	86.6	3.9	801	5	AAS90729	Aas90729 DNA encod
25	85.4	3.8	3399	2	AAT05868	Aat05868 Chicken 1
26	84.6	3.8	708	5	AAS69547	Aas69547 DNA encod
27	84.6	3.8	708	5	AAS75461	Aas75461 DNA encod
28	83.8	3.8	441	5	AAS75453	Aas75453 DNA encod
29	83.8	3.8	1684	5	AAS90724	Aas90724 DNA encod
30	83.8	3.8	29392	2	AAV15422	Aav15422 Mouse pol
C 31	83.4	3.7	49999	2	AAS23895	Aaz23895 Murine LO
32	83.2	3.7	372	5	AAS75452	Aas75452 DNA encod
33	83	3.7	393	5	AAS90684	Aas90684 DNA encod
34	83	3.7	96596	8	ADA02564	Ada02564 Human RAS
35	83	3.7	96596	9	ADB72302	Adb72302 Human RAS
36	82.6	3.7	309	5	AAS71089	Aas71089 Probe #25
C 37	82.2	3.7	496	4	AAI12609	Aai12609 Human foe
C 38	82.2	3.7	496	4	ABA54309	Aba54309 Human bre
C 39	82.2	3.7	496	4	AAI33960	Aai33960 Probe #26
C 40	82.2	3.7	496	4	ABA43847	Aba43847 Human bre
C 41	82.2	3.7	496	4	ABA4068	Aba24068 Probe #25
C 42	82.2	3.7	496	4	AAK28026	Aak28026 Human bon
C 43	82.2	3.7	496	4	AAK02592	Aak02592 Human bra
C 44	82.2	3.7	496	4	ABS27626	Abs27626 Human liv
C 45	82.2	3.7	496	5	AAI02512	Aai02512 Probe #25

ALIGNMENTS

RESULT 1  
AAX23321  
ID AAX23321 standard; cDNA; 2226 BP.  
XX  
AC AAX23321;  
XX  
DT 11-JUN-1999 (first entry)  
XX  
DE N. meningitidis strain H44/76 LbpB cDNA.  
XX  
KW lbpB; lactoferrin binding protein; vaccine; neisserial disease;  
KW meningitis; diagnosis; treatment; ds.  
XX  
OS Neisseria meningitidis.  
XX  
FH Location/Qualifiers  
CDS 1..2226  
FT /\*tag= a  
FT /product= "LbpB"  
XX  
PN WO9909176-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 10-AUG-1998; 98WO-RP005117.  
XX  
PR 15-AUG-1997; 97GB-00017423.  
PR 05-FEB-1998; 98GB-00002544.  
XX  
PA (UYUT-) RIJXSUNIV UTRECHT.  
PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.  
XX  
PI Pettersson-Fernholm AM, Tommassen JPM;  
XX  
DR WPI; 1999-190165/16.  
DR P-PSDB; AAW93494.  
XX  
PT New lactoferrin-binding protein B polynucleotides - obtained from  
PT Neisseria meningitidis, used to develop products for the diagnosis,  
PT prevention and treatment of neisserial disease, e.g. meningitis.  
XX  
PS Claim 2; Page 90-94; 116pp; English.  
XX  
CC This invention describes novel lactoferrin-binding protein B (lbpB)  
CC strains of Neisseria meningitidis. The products of this invention can be  
CC used for vaccinating humans against neisserial disease e.g. meningitis.

Handwritten signature: *App. 10/07*

CC Antibodies raised against the proteins of the invention can be used for  
 CC diagnosing or treating neisserial disease in humans. The lbpB  
 CC polypeptides can also be used for identifying compounds which inhibit the  
 CC polypeptides

XX Sequence 2226 BP; 683 A; 483 C; 571 G; 489 T; 0 U; 0 Other;

Query Match 100.0%; Score 2226; DB 2; Length 2226;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGTGTAACCGGAATATGCGCGCATTTGCTGTTGGCCCTACTTTTGGCATCTTGTAAT	60
Db	1	ATGTGTAACCGGAATATGCGCGCATTTGCTGTTGGCCCTACTTTTGGCATCTTGTAAT	60
Qy	61	GGCGGCAATTTCCGCGTGCAGCTGTTGTCGAATCAACGCCGACCGCGTACCCCGTCAC	120
Db	61	GGCGGCAATTTCCGCGTGCAGCTGTTGTCGAATCAACGCCGACCGCGTACCCCGTCAC	120
Qy	121	TTCAAGTCTAAGACGTTCCACTCCGCCCTCCGCTGCGCAACCTTCTATAGAAACACGCGG	180
Db	121	TTCAAGTCTAAGACGTTCCACTCCGCCCTCCGCTGCGCAACCTTCTATAGAAACACGCGG	180
Qy	181	GTGCGGTCAACCGGCGCTGCGTGGTGGCGCAATGCGGCTGTTGAGCGGGAATTTTCGCA	240
Db	181	GTGCGGTCAACCGGCGCTGCGTGGTGGCGCAATGCGGCTGTTGAGCGGGAATTTTCGCA	240
Qy	241	ACTTCTGATAGGTGTCGCAATGATTTTCCAAATAGCAAAACAGCAGAGAAAGCTGTG	300
Db	241	ACTTCTGATAGGTGTCGCAATGATTTTCCAAATAGCAAAACAGCAGAGAAAGCTGTG	300
Qy	301	TTTAAAGAGGTGATGTTCTGTTTATACGTTTCAAAAAGATAAATTCAGTGGCTT	360
Db	301	TTTAAAGAGGTGATGTTCTGTTTATACGTTTCAAAAAGATAAATTCAGTGGCTT	360
Qy	361	AAGGATAAAATTCATCAACGCAATCTTAATGTAGAAATTAGGACATCAGAAATGAAAT	420
Db	361	AAGGATAAAATTCATCAACGCAATCTTAATGTAGAAATTAGGACATCAGAAATGAAAT	420
Qy	421	AAAAAATATGTTATGAATTTGTGGATGCGGTTATGTAATATCTAAAAACGGAACAGAT	480
Db	421	AAAAAATATGTTATGAATTTGTGGATGCGGTTATGTAATATCTAAAAACGGAACAGAT	480
Qy	481	GAAATTCAGTGGCACTTCAATTCGCAAGCAGTTTCTAATCGTTTGGTACGAGCGTTT	540
Db	481	GAAATTCAGTGGCACTTCAATTCGCAAGCAGTTTCTAATCGTTTGGTACGAGCGTTT	540
Qy	541	GTATATATTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGGAAACGGTCAATAT	600
Db	541	GTATATATTCGGAGAACATCTTCCCAATCTTTACCGAGCGGGGAAACGGTCAATAT	600
Qy	601	TCCGGTAATCGCAATATATGACCGATGCCATAGCTCATCGAAACAGAAACGAGGAT	660
Db	601	TCCGGTAATCGCAATATATGACCGATGCCATAGCTCATCGAAACAGAAACGAGGAT	660
Qy	661	CCTAGCGAAGATTTGGGTATCTCGTTTATACGTTCAAAATGTCGGAGCACTTCTTAT	720
Db	661	CCTAGCGAAGATTTGGGTATCTCGTTTATACGTTCAAAATGTCGGAGCACTTCTTAT	720
Qy	721	GCTGCACTGCGCAGACCGGGAGGAAAAACATCTCGCGGAATATACGTTGATTCGAT	780
Db	721	GCTGCACTGCGCAGACCGGGAGGAAAAACATCTCGCGGAATATACGTTGATTCGAT	780
Qy	781	AAGAAAACTTTGACGGGTCAATTAATTAATAATAGTATGTCGCAAAAGAACCGATGAA	840
Db	781	AAGAAAACTTTGACGGGTCAATTAATTAATAATAGTATGTCGCAAAAGAACCGATGAA	840
Qy	841	AAGAAACCACTGACCATTTACGACATTCAGCAATTTGGAACGCAACCGCTTTACCGG	900
Db	841	AAGAAACCACTGACCATTTACGACATTTACGCAATTTGGAACGCAACCGCTTTACCGG	900
Qy	901	AGTGCACAAAGTTAAACCGAGTTGAAGACGACCGCTGATTAAGAGCATTTGTTTTC	960
Db	901	AGTGCACAAAGTTAAACCGAGTTGAAGACGACCGCTGATTAAGAGCATTTGTTTTC	960

Db	901	AGTGCACAAAGTTAAACCGAGTTGAAGACGACCGCTGATTAAGAGCATTTGTTTTC	960
Qy	961	CATACCGATCGCGATCAGCGCTTGAGGCGGTTTTTTTCGGCGATAAGGGGGAAGAGCTT	1020
Db	961	CATACCGATCGCGATCAGCGCTTGAGGCGGTTTTTTTCGGCGATAAGGGGGAAGAGCTT	1020
Qy	1021	GCGGACGGTTTTATCAGCAACGACACAGCGTATTTCGGCGTATTCGAGGCAAAAAACA	1080
Db	1021	GCGGACGGTTTTATCAGCAACGACACAGCGTATTTCGGCGTATTCGAGGCAAAAAACA	1080
Qy	1081	AAGCATCAAAACGACAGATACAAATCTGCTATGCTGCTGAAAAACACACCAAAATC	1140
Db	1081	AAGCATCAAAACGACAGATACAAATCTGCTATGCTGCTGAAAAACACACCAAAATC	1140
Qy	1141	TTGGAATCTCTGAAAAATTTCCGTTGACGAGGCGACGATAAAAAATGCCCGCTTTGCC	1200
Db	1141	TTGGAATCTCTGAAAAATTTCCGTTGACGAGGCGACGATAAAAAATGCCCGCTTTGCC	1200
Qy	1201	ATTTCCTCTGCTCCGATTTTGGCCATCCCGACAAATCTCTGTCGAGGGGCGTGAAT	1260
Db	1201	ATTTCCTCTGCTCCGATTTTGGCCATCCCGACAAATCTCTGTCGAGGGGCGTGAAT	1260
Qy	1261	CTTTGGTTAGCAAGAGAAACCATCGAGCTTCCGACGCGAGGAAATGACCGTCCGT	1320
Db	1261	CTTTGGTTAGCAAGAGAAACCATCGAGCTTCCGACGCGAGGAAATGACCGTCCGT	1320
Qy	1321	GCTTGTTCGATTTTCTGACCTATGTGAACTCGGACGCGATAAAAACTGACCGCCACGA	1380
Db	1321	GCTTGTTCGATTTTCTGACCTATGTGAACTCGGACGCGATAAAAACTGACCGCCACGA	1380
Qy	1381	AGTAAACCAAGCGGGAAGATAAAGGAAAGATGAAGAGGATACAGGGTGTGTAAGAC	1440
Db	1381	AGTAAACCAAGCGGGAAGATAAAGGAAAGATGAAGAGGATACAGGGTGTGTAAGAC	1440
Qy	1441	GAAGAGGACGAGAGATGAGCGCGAGAGGCGAGCGAGGAGCGAGGAGGAGGAGGAG	1500
Db	1441	GAAGAGGACGAGAGATGAGCGCGAGAGGCGAGCGAGGAGCGAGGAGGAGGAGGAG	1500
Qy	1501	GATGAAGGAGGAGTGCAGAGAGCAAGCGCGAGAAAAACGAAAGCGCGAGAGAGAG	1560
Db	1501	GATGAAGGAGGAGTGCAGAGAGCAAGCGCGAGAAAAACGAAAGCGCGAGAGAGAG	1560
Qy	1561	GCTGAAGAACTCTGAAGAACCCGAGAGAGATTCGCGCGGAGAGCGGGGCGGTGTTCA	1620
Db	1561	GCTGAAGAACTCTGAAGAACCCGAGAGAGATTCGCGCGGAGAGCGGGGCGGTGTTCA	1620
Qy	1621	GACGGCATCTGCGCGCTCCGAGAGCTCTTAAAGGAGGAGGATATCGACCTTTCTGAAA	1680
Db	1621	GACGGCATCTGCGCGCTCCGAGAGCTCTTAAAGGAGGAGGATATCGACCTTTCTGAAA	1680
Qy	1681	GATATCGCAGCGGAGAGCGGACATTCGCAAACTGGAAGAGCACTATACCGGCACT	1740
Db	1681	GATATCGCAGCGGAGAGCGGACATTCGCAAACTGGAAGAGCACTATACCGGCACT	1740
Qy	1741	TGGGAAGCGGATATCAGCAAAACCATTCATATGGAAGCAATCATGCGGATATAAAGGCG	1800
Db	1741	TGGGAAGCGGATATCAGCAAAACCATTCATATGGAAGCAATCATGCGGATATAAAGGCG	1800
Qy	1801	AAAGCAGAAATTTGAGCTTGAATTCGGCGAGAAATCGATTCGGGAAACGCTGACGAGAA	1860
Db	1801	AAAGCAGAAATTTGAGCTTGAATTCGGCGAGAAATCGATTCGGGAAACGCTGACGAGAA	1860
Qy	1861	AACGGTGTACAACTGCTTTCCATATTTGAAACCGCGCTGATTGAGGGCAATGGTTTCCAC	1920
Db	1861	AACGGTGTACAACTGCTTTCCATATTTGAAACCGCGCTGATTGAGGGCAATGGTTTCCAC	1920
Qy	1921	GGGACAGCGGCACTCGGGATTAACGGCATCAATCTTTTCGGGAAATGATTCGACTAATCCT	1980
Db	1921	GGGACAGCGGCACTCGGGATTAACGGCATCAATCTTTTCGGGAAATGATTCGACTAATCCT	1980
Qy	1981	CCAGTTTCAAGGCGCAATTAATCTTCTGTAACAGGCGGCTTTTACGGCCCGCAGCGGAG	2040
Db	1981	CCAGTTTCAAGGCGCAATTAATCTTCTGTAACAGGCGGCTTTTACGGCCCGCAGCGGAG	2040

QY 2041 GAATGGCGGTACTATTTCATTAATGATGGGAATCTCTGGTATTAACGATGACT 2100  
 Db |||||  
 QY 2041 GAATGGCGGTACTATTTCATTAATGATGGGAATCTCTGGTATTAACGATGACT 2100  
 Db |||||  
 QY 2101 GAAATGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 2160  
 Db |||||  
 QY 2101 GAAATGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 2160  
 Db |||||  
 QY 2161 GAAGCTAAACCCCAATTCGGCTGGTATTCGGTGGCAAGAGATAATAAGAGCTGGAA 2220  
 Db |||||  
 QY 2161 GAAGCTAAACCCCAATTCGGCTGGTATTCGGTGGCAAGAGATAATAAGAGCTGGAA 2220  
 Db |||||  
 QY 2221 AAATGA 2226  
 Db |||||  
 QY 2221 AAATGA 2226

## RESULT 2

ACA41945  
 ID ACA41945 standard; DNA; 2226 BP.

AC ACA41945;

DT 19-JUN-2003 (first entry)

DE Prokaryotic essential gene #21602.

KW Antisense; ds; prokaryotic essential gene; cell proliferation;  
 drug design; gene.

OS Neisseria meningitidis.

PN WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107

XX 21-MAR-2001; 2001US-00815247.

XX 06-SEP-2001; 2001US-00948953.

XX 25-OCT-2001; 2001US-0342943P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0342599P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-PSDB; ABU38075.

XX New antisense nucleic acids, useful for identifying proteins or screening  
 for homologous nucleic acids required for cellular proliferation to  
 isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 29815; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
 the 6213 antisense sequences given in the specification where expression  
 of the nucleic acid inhibits proliferation of a cell. Also included are:  
 (1) a vector comprising a promoter operably linked to the nucleic acid  
 encoding a polypeptide whose expression is inhibited by the antisense  
 nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 polypeptide or its fragment whose expression is inhibited by the  
 antisense nucleic acid; (4) an antibody capable of specifically binding  
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 proliferation or the activity of a gene in an operon required for  
 the gene product or that has an activity against a biological pathway  
 required for proliferation, or that inhibits cellular proliferation; (8)  
 identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies  
 or a gene on which the test compound that inhibits proliferation of an  
 organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 compound's activity; (11) a culture comprising strains in which the gene  
 product is overexpressed or underexpressed; (12) determining the extent  
 to which each of the strains is present in a culture or collection of  
 strains; or (13) identifying the target of a compound that inhibits the  
 proliferation of an organism. The antisense nucleic acids are useful for  
 identifying proteins or screening for homologous nucleic acids required  
 for cellular proliferation to isolate candidate molecules for rational  
 drug discovery programs, or for screening homologous nucleic acids  
 required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
*X. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 2226 BP; 701 A; 466 C; 566 G; 493 T; 0 U; 0 Other;

Query Match 79.7%; Score 1774.8; DB 7; Length 2226;  
 Best Local Similarity 88.4%; Pred. No. 0;

Matches 1990; Conservative 0; Mismatches 212; Indels 48; Gaps 4;

QY 1 ATGTGTAACCGAATTATGGCGCAATTGTCTTGTTCCTTACTTTTGGCACTTTGTATT 60

Db 1 ATGTGTAACCGAATTATGGCGCAATTGTCTTGTTCCTTACTTTTGGCACTTTGTATT 60

QY 61 GGCGGCAATTTCGGCGTGCAGCTTGTTCGAATCAACGCGGACGGGTACCCGTCAT 120

Db 61 GGCGGCAATTTCGGCGTGCAGCTTGTTCGAATCAACGCGGACGGGTACCCGTCAT 120

QY 121 TTCAAGTCTAAGGACGTTTCCCACTCCGCCCTCCCAACCTTCTATAGAACACGCGC 180

Db 121 TTCAAGTCTAAGGACGTTTCCCACTCCGCCCTCCCAACCTTCTATAGAACACGCGC 180

QY 181 GTGCCGTCAACCGGCTTGCCTGCGTGGCGCAATCGGCTGTGTAGCGGATTTTGCSCA 240

Db 181 GT-----CAACCGGCTGCGTGGCGCAATCGGCTGTGTAGCGGATTTTGCSCA 240

QY 241 ACITCTGATAGTTGGCAATGATTTTCCAAATAGCAAAACAAGCAGAGAAAAGCTGTG 300

Db 241 ACITCTGATAGTTGGCAATGATTTTCCAAATAGCAAAACAAGCAGAGAAAAGCTGTG 300

QY 235 TTTCATCGTAGAGATGCGCAATTCGCGATAGCAAAACAAGCAGAGAAAAGCTGTG 294

Db 235 TTTCATCGTAGAGATGCGCAATTCGCGATAGCAAAACAAGCAGAGAAAAGCTGTG 294

QY 301 TTTAAGAGAGTGATGTTCTGTTTATACGGTTTCAAAAAGATAAATCTTCACTGGCTT 360

Db 295 TTTAAGAGAGTGATGTTCTGTTTATACGGTTTCAAAAAGATAAATCTTCACTGGCTT 354

QY 361 AAGGATAAAATTCATCAACGCAATCCTTAATGTAGAAATAGGACATCAGAAAATGAAAAT 420

Db 355 AAGGATAAAATTCATCAACGCAATCCTTAATGTAGAAATAGGACATCAGAAAATGAAAAT 414

QY 421 AAAAAATATGTTATGAAATTTGCGATCGCGTATGTATATATATACTATAAAGCAAGAT 480

Db 415 AAAAAATATGTTATGAAATTTGCGATCGCGTATGTATATATACTATAAAGCAAGAT 474

QY 481 GAAATTTAGTGGACTTCAAAATCGCAAGCAATCTTAATCGTTTTCGCTACGACGTTTT 540

Db 475 GAAATTTAGTGGACTTCAAAATCGCAAGCAATCTTAATCGTTTTCGCTACGACGTTTT 534

QY 541 GTATATTTTCGGAGAAATCCTTCCCAATCTTTTACCGAGCGCGGGAACGGTCAATAT 600

Db 535 GTATATTTTCGGAGAAATCCTTCCCAATCTTTTACCGAGCGCGGGAACGGTCAATAT 594

QY 601 TCGGTAACTGGCAATATATGACCGATGCGATCGTATCGAACAGAGAAAAGCAGAGAT 660

Db 595 TCGGTAACTGGCAATATATGACCGATGCGATCGTATCGAACAGAGAAAAGCAGAGAT 654

QY 661 CTTAGCAAGATTTGGGTTTATCTCGTTTATACGGTCAAAAATGTCGAGCACTTCTTAT 720

Db 655 CTTAGCAAGATTTGGGTTTATCTCGTTTATACGGTCAAAAATGTCGAGCACTTCTTAT 714

QY 721 GCTGCACTGCGCAGCAGCGGAGGAAACATCTCTGCCGAATATACGGTTGATTTTCGAT 780



Db 715 GCTGCGATCCGACGACGAGGAGAAACATCTCCGGAATATACGCTAGATTCCGCT 774  
Qy 781 AAGAAACCTTTGACGGCTCAATTAATTAATAATCAGTATGTGCAAAAGAAACCGATGAA 840  
Db 775 AAGAAACCTTTGACGGCTCAATTAATTAATAATCAGTATGTGCAAAAGAAACCGATGAA 834  
Qy 841 AAGAAACCTTTGACGGCTCAATTAATTAATAATCAGTATGTGCAAAAGAAACCGATGAA 900  
Db 835 AAGAAACCTTTGACGGCTCAATTAATTAATAATCAGTATGTGCAAAAGAAACCGATGAA 894  
Qy 901 AGTCCCAAGTTTACACCGAGTTCAAGACGAGCCAGCTGATTAAGAGCATTTGTTTTTC 960  
Db 895 AGTCCCAAGTTTACACCGAGTTCAAGACGAGCCAGCTGATTAAGAGCATTTGTTTTTC 954  
Qy 961 CATACCGATGCGATCAGCGCTTTGAGGGCGGTTTTTTCGCGATAGGGGGAAGAGCTT 1020  
Db 955 CATACCGATGCGATCAGCGCTTTGAGGGCGGTTTTTTCGCGATAGGGGGAAGAGCTT 1014  
Qy 1021 GCCGACGCTTTATCAGCAACGACACACAGCGTATTCGCGTATTCGCAAGCA---AAAA 1077  
Db 1015 GCCGACGCTTTATCAGCAACGACACACAGCGTATTCGCGTATTCGCAAGCA---AAAA 1074  
Qy 1078 ACAAACGATCAAAACGACGAGATCAAAATCCTGCTATGCGCTCTGAAAAACACACCAAA 1137  
Db 1075 ACAGACGATCAAAACGACGAGATCAAAATCCTGCTATGCGCTCTGAAAAACACACCAAA 1134  
Qy 1138 ATCTTGGATCTCTGAAATTTCCGTTGACGAGCGACGATTAATAATGCGCGCGGTTT 1197  
Db 1135 ATCTTGGATCTCTGAAATTTCCGTTGACGAGCGACGATTAATAATGCGCGCGGTTT 1194  
Qy 1198 GCCATTTCCCTCTGCCGATTTTGGCCATCCGACAACTCTTGTGCAAGGGCGTGAA 1257  
Db 1195 GCCATTTCCCTCTGCCGATTTTGGCCATCCGACAACTCTTGTGCAAGGGCGTGAA 1254  
Qy 1258 ATCTCTTGGTTAGCCAGAGAAACCATCGAGCTTGCAGCGCGAGGAAATGACCGTC 1317  
Db 1255 ATCTCTTGGTTAGCCAGAGAAACCATCGAGCTTGCAGCGCGAGGAAATGACCGTC 1314  
Qy 1318 CGTCTGTTGCGATTTTCTGACCTATGTAACCTCGGACGGAATAAACTGACCGCCA 1377  
Db 1315 AGTCTGTTGCGATTTTCTGACCTATGTAACCTCGGACGGAATAAACTGACCGCCA 1374  
Qy 1378 GCAAGTAAACCAAGCGCGAGATAAA-----GGGAAGATGAA 1416  
Db 1375 GCAAGTAAACCAAGCGCGAGATAAAATTCGGAAGATGAAATTTGGTGAAGCGAGAA 1434  
Qy 1417 GAGGATACAGCGCTTGTGTAACGACGAAGAGCGACGAGATGAAGCGGAGCGAGC 1476  
Db 1435 AATGAAGAGATTTGTCGCTGAAGAGAAACACGGAAGACGAAGTCTGTAAGATGAA 1494  
Qy 1477 GAAGGAGCGAGAGAGAAATCGCGATGAAGGAGAGGTGCGGAAGAGAGAGCGCGAGAA 1536  
Db 1495 GACAGAGAGAGAGAGAGATTTCCGAGATGTAACAGTGAAGAGAGAGAGAGAAATCGCC 1554  
Qy 1537 AACGAGCGCGAGAGAGAGAGATGTAAGAGCTGAGAGACCTGAGAGACCGGAGAGAAATCGCG 1596  
Db 1555 GAAGAAGATGATGAAGCGCGAGAGAGAGATGTAAGAGCTGAGAGACCGGAGAGAAATCGCG 1614  
Qy 1597 GCAGAGAGCGCGGCTGTTGTTGTTGAGAGCGGATCTGCGCGCTCCGAGAGCTCTAAAGC 1656  
Db 1615 GAAGAAGCGCGGCTGTTGTTGTTGAGAGCGGATCTGCGCGCTCCGAGAGCTCTAAAGC 1674  
Qy 1657 AGGATATCGACCTTTCTGAAAGGTATCCGACGCGGAGAGCGGATCTCGCAACT 1716  
Db 1675 AGGACATCGACCTTTCTGAAAGGTATCCGACGCGGAGAGCGGATCTCGCAACT 1734  
Qy 1717 GGAAGACGAGCTATACCGGACTTTGGGAGCGGATATCAGCAAAACCCATTAATGGGAC 1776  
Db 1735 GGAAGACGAGCTATACCGGACTTTGGGAGCGGATATCAGCAAAACCCATTAATGGGAT 1794  
Qy 1777 AATCATGCGGATAAAAAGCGCAAAAGCAGAAATTTGACGTTGATTTCCGCGAGAAATCG 1836

Db 1795 AATAAGCGCGATAAAAAGCGCAAAAGCAGAAATTTGACGTTGATTTTCGCGAGAAATCG 1854  
Qy 1837 ATTTCCGGAAGCTGACGAGAGAAACCGGTGTAACAACCTGTTTCCCATATTGAAAAACGCG 1896  
Db 1855 ATTTCCGGAAGCTGACGAGAGAAACCGGTGTAACAACCTGTTTCCCATATTGAAAAAGGT 1914  
Qy 1897 GTGATTTGAGGCGCAATGTTTCCACGCGACAGCGCGCACTCGGGATAACGGCATCAATCTT 1956  
Db 1915 GTGATTTGAGGCGCAATGTTTCCACGCGACAGCGCGCACTCGGGATAACGGCATCAATCTT 1974  
Qy 1957 TCGGGAATGATTCGCACTAATTCCTCCAAAGTTTCAAGCCCAATATCTTCTTGTACAGGC 2016  
Db 1975 TCGGGAATGATTCGCACTAATTCCTCCAAAGTTTCAAGCCCAATATCTTCTTGTACAGGC 2034  
Qy 2017 GGCTTTTACGCGCGCGAGCGGAGGAAATTCGGCGGTACTATTTTCAATTAATGATGGGAAA 2076  
Db 2035 GGATTTTACGCGCGCGAGCGGAGGAAATTCGGCGGTACTATTTTCAATTAATGATGGGAAA 2094  
Qy 2077 TCTCTTGTATATACTGAAGATACTGAAAAATGAAGCTGAAGCTGAAGTTGAAAAATGAAGCT 2136  
Db 2095 TCTCTTGTATATACTGAAGATATTGACAA-----TGAATTTGAAGCT 2136  
Qy 2137 GGTGTTGCGGAGCACTTAAACCTGAAGCTTAAACCCCAATTCGGCGGTGTTTTCGGTCG 2196  
Db 2137 GATGCTGCGGAGCACTTGAACCTGAAGCTTAAACCCCAATTCGGCGGTGTTTTCGGTCG 2196  
Qy 2197 AAGAAAGATATAAGAGGTGGAATAATGA 2226  
Db 2197 AAAAAAGATATGAGGAGGTGGAATAATGA 2226

RESULT 3  
AAX23323  
ID AAX23323 standard; cdna; 2124 BP.  
XX  
AC AAX23323;  
XX  
DT 11-JUN-1999 (first entry)  
XX  
DE N. meningitidis strain 881607 LbpB cdna.  
XX  
LbpB; lactoferrin binding protein; vaccine; neisserial disease;  
KW meningitis; diagnosis; treatment; ds.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2124  
FT /tag= a  
FT /product= "LbpB"  
XX  
FN WO9909176-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 10-AUG-1998; 98WO-EP005117.  
XX  
PR 15-AUG-1997; 97GB-00017423.  
PR 05-FEB-1998; 98GB-00002544.  
XX  
XX (UYUT-) RIJKSUNIV UTRECHT.  
(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.  
XX  
PI Pettersson-Fernholm AM, Tommaassen JPM;  
XX  
DR WPI; 1999-190165/16.  
DR P-PSDB; AAW93496.  
XX  
XX New lactoferrin-binding protein B polynucleotides - obtained from  
PT Neisseria meningitidis, used to develop products for the diagnosis,  
PT prevention and treatment of neisserial disease, e.g. meningitis.  
XX  
PS Claim 2; Page 105-109; 116pp; English.

*Applied*

XX This invention describes novel lactoferrin-binding protein B (LbpB) strains of *Neisseria meningitidis*. The products of this invention can be used for vaccinating humans against neisserial disease e.g. meningitis. CC Antibodies raised against the proteins of the invention can be used for CC diagnosing or treating neisserial disease in humans. The LbpB CC polypeptides can also be used for identifying compounds which inhibit the CC polypeptides

XX  
SQ Sequence 2124 BP; 663 A; 461 C; 541 G; 459 T; 0 U; 0 Other;

Query Match 67.4%; Score 1499.8; DB 2; Length 2124;  
Best Local Similarity 83.3%; Pred. No. 0;  
Matches 1779; Conservative 0; Mismatches 317; Indels 39; Gaps 5;

QY 1 ATGTGTAACCGAATATGGCGGCAATGTCTGTGGCCCTTACTTTTGGCACTTTGTATT 60  
DB 1 ATGTGTAACCGAATATGGCGGCAATGTCTGTGGCCCTTACTTTTGGCACTTTGCATC 60

QY 61 GGCGCAATTTCCGGGTGCGAGCTGTGTGCAATCAACGCCACCGCTTACCCCGTCACT 120  
DB 61 GGCGCAATTTCCGGGTGCGAGCTGTGTGCAATCAACGCCACCGCTTACCCCGTCACT 120

QY 121 TTCAAGTCTAAGGAGCTTTCCCACTCCGCCCTCGCCCAACCTTCTATAGAAACACACGCG 180  
DB 121 TTCAAGTCTAAGGAGCTTTCCCACTTCGCTCTCTGCGGGTCTTCGGTAGAAACACACGCG 180

QY 181 GTGCGGTCAACCGGCGCTCGCTGCGGTGCGGCAATGCGGCTGTGAGCGGATTTGCA 240  
DB 181 GT-----CAACCGGCGGCGCTGTGCGGCAATGCGGCTGTGAGCGGCAATTTGCA 234

QY 241 ACTTCTGATAAGTGTGGCAATGATTTTCCAAATAGCAACACGAGCAAGAAAGCTGTG 300  
DB 235 ACTTCTGATAAGTGTGGCAATGATTTTCCAAATAGCAACACGAGCAAGAAAGCTGTG 294

QY 301 TTTAAGAGGTGATGTCTGTTTTTATACGGTTTCAAAAAAGATAAACTTCAGTGGCTT 360  
DB 295 TTTAAGAGGAGATATCTCTGTTTTATACGGTTTCCAAAGAGATCAACGTACAGCTT 354

QY 361 AAGATATAATTCATCAACGCAATCTTACGCAAGCAATTTAGGATCAGAAATGAAAT 420  
DB 355 AAGATATAATTCGTCACCAAACTTACGCAAGCAATTTAGGATCAGAAATGAAAT 414

QY 421 AAAAAATATGTTATGAATTTGCGATGCGGTTATGTATATCTTAAAGACGGAACAGAT 480  
DB 415 AAAAAATATGTTATGAATTTGCGATGCGGTTATGTATATCTTAAAGACGGAACAGAT 474

QY 481 GAAATGAGTGGACTTCAAAATCGCAAGCAGTTTTCTAATCGTTTTTGGCTACGACGGTTT 540  
DB 475 GAAATGAGTGGACTTCAAAATTAACAGCAGTCTACCAACCGTTTTGTTATGACGGTTT 534

QY 541 GTATATTTTCCGGAGAACATCTTCCCAATCTTTACGAGCGCGGAAACGGTGCAATAT 600  
DB 535 GTATATTTTCCGGAGAACATCTTCCCAATCTTTACGAGCGCGGAAACGGTGCAATAT 594

QY 601 TCCGTAACCTGGCAATATATGACGATGCGATAGCTCATCGAACAGAAAGACGAGAT 660  
DB 595 TCCGTAACCTGGCAATATATGACGATGCGATAGCTCATCGAACAGAAAGACGAGAT 654

QY 661 CTAGCGAAGATTTGGGTTATCTCGTTTTATAGCGTCAAAATGTGCGAGCAATCTTCTAT 720  
DB 655 CTAGCGAAGATTTGGGTTATCTCGTTTTATAGCGTCAAAATGTGCGAGCAATCTTCTAT 714

QY 721 GCTGCGACTCCGACGACCGGAGGGAACATCTCTGCGCAATATACGGTTGATTTGAT 780  
DB 715 GCTGCGACTCCGACGACCGGAGGGAACATCTCTGCGCAATATACGGTTGATTTGAT 774

QY 781 AAGAAAATTTTGAGCGGTCAATTAATTTAAATTCAGTATGTGCAAGAAACCGATGAA 840  
DB 775 CAAAAAATCTGAAATGGCAAGCTGATTAATAATTTAGTATGTGCAAGAAAGAGATGATCCT 834

QY 841 AAGAAAATCTGACCAATTTACGACATTTACGCAACATTTGACGCGCAACCGCTTTACCGC 900  
DB |||||

DB 835 AAAAAACCACTGACCATTTTACGACATTTACTGCAAAATTTGACGCGCAACCGCTTTACCGGC 894  
QY 901 AGTGCCAAAGTTTAAACACCGAGTTGAAGACGAGCCAGCTGATAAGAGCATTTGTTTTTC 960  
DB 895 AGTGCCAAAGTTTAAACACGAGGTGAAGAGCAATCAACGCTGATAAGAGCAATTTGTTTTTC 954  
QY 961 CATACGATGCGCATCAGCGGCTTGAAGGCGGTTTTTTTCGGCGATAAGGCGGAAGAGCTT 1020  
DB 955 CATACGATGCGCATCAGCGGCTTGAAGGCGGTTTTTTTCGGCGATAAGGCGGAAGAGCTT 1014

QY 1021 GCGGACCGTTTTATCAGCAACGACAAACAGCGTATTTCGGCGTATTTCGAGCA---AAAAA 1077  
DB 1015 GCGGACCGTTTTATCAGCAACGACAAACAGCGTATTTCGGCGTATTTCGAGCAACCAAAA 1074

QY 1078 ACACACCGCATCAACCGCAGCAGATACAAATCCTGCTATGCTGCTGTAAGAAACACACCAA 1137  
DB 1075 ACAGAGCAGCAACGCAATCAGATACAAATCCTGCTGCTGCTGTAAGAAACACACCAA 1134

QY 1138 ATCTTGGATTTCTGAAAAATTTCCGTTGACGAGCGCAGGATATAAAATGCGCGCGCTTT 1197  
DB 1135 ATCTTGGATTTCTAAAAATTTCCGTTGACGAGCAAGTGTGAAATTCCTCGACCGTTT 1194

QY 1198 GCCATTTCCCTCTGCGCGATTTTGGCCATCCCGCAAAACTCTTGTTCGAAGGCGTGAA 1257  
DB 1195 GAGGTTTCCATATGCCCGATTTTGGTCATCCCGCAAAACTTCTTGTGGAAGGCGTGAA 1254

QY 1258 ATTCTTTGGTTAGCAAGAGAAAAACCATCTGAGCTTCCGACGCGCAGGAAATGACCGTC 1317  
DB 1255 ATTCTTTGGTTAGCAAGAGAAAAACCATCTGAGCTTCCGACGCGCAGGAAATGACCGTC 1314

QY 1318 CGTCTTGTTCGACTTTTTCGACCTATGTGAAACTCTCGACGGAATAAACTGACCGCCA 1377  
DB 1315 CGTCTTGTTCGACTTTTTCGACCTATGTGAAACTCTCGACGGAATAAACTGACCGCCC 1374

QY 1378 GCAAGTAAACCAAGGCGGAAGATTAAGGAGAGATGAAGAGATACAGCGTTTGGTAAC 1437  
DB 1375 GCGTCCAAACGGAAGGCGGAGATGAAGAGGAGGAGCAAGAGAGGTGTAGGCGTTGATAAC 1434

QY 1438 GACCAAGAGCAGCGGAGATGAAGCGCAGAGGCGCAGGAGCGAGGAGCGGAGCAATC 1497  
DB 1435 GGTAAAGAGCGGAGAGCAAAATCGCGATGAAGAAAGCACCAGGAGCAAGTCTAGAA 1494

QY 1498 GCGCATGAAGAGAGGTGCGGAGAGCAAGACCGCCAGAAACGAAAGCGCGCAAGAGAGAC 1557  
DB 1495 GATGAAGCAGAGATGAAGACGGAAGAAATCGAAGAA-----GAACCTGAA 1542

QY 1558 GAAAGTGAAGAACTGAGAACCCGAGAGAGATCGCGCGCAGAGAGCGCGGTGGTGGT 1617  
DB 1543 GAAGAGCTGAAGAGAGAAACCCGAGAGAAATTCGCGCAGAGAAAGCAACGCGCGGT 1602

QY 1618 TCAGACGGCATCTCTGCGCGCTCCGGAAGCTCTTAAAGGACGAGGATTCGACCTTTTCTG 1677  
DB 1603 TCAGGACGATCTCTGCGCGCTCCGGAAGCTCTTAAAGGACGAGGATTCGACCTTTTCTG 1662

QY 1678 AAGGTTATCCGACGCGGAGCCGACATTCGCAAACTGGAAAAAGCACCTATACCGGC 1737  
DB 1663 AAGGTTATCCGACGCGGAGCCGACATTCGCAAACTGGAAAAAGCACCTATACCGGC 1722

QY 1738 ACTTGGAGCGGTATCAGCAAC-----CCATTCAATGGGCAATCAT 1782  
DB 1723 ACTTGGAGCGGTATCAGCGGTATCGGATAGTGTGATCGCTCCATTCAAAGGATAGCTAT 1782

QY 1783 GCGATATAAAGCGGCAAAAGCAGAAATTTGAGTTGATTTCCGCGAGAAATCGATTTCC 1842  
DB 1783 GCG---AATCAAGGGCAAAAGCAGAAATTTACGTTGATTTGGAAGCGAGCGGTGTC 1839

QY 1843 GGAACGCTCAGCGAGAAAAACCGTGTACAACTGCTTTCCATATTTGAAACCGCGTGATT 1902  
DB 1840 GGAATGCTCAGCAGAAAAAATGATACAACTCCCGCTTTTATATTGAAAAAGGTGATT 1899

QY 1903 GAGGCAATGTTTCCACGCGACGCGCACTCGGAGTAAACCGCATCAATCTTTTCGGA 1962  
DB 1900 GACGCTAACCGTTTCCACGCTTTTGGCGCATACTCGGAGAAACGGTATTGACCTTTCTGG 1959

	1963	AATGATTCCGACTTAATCTTCCCAAGTTTCAAAGCCAATAATCTTCTTGTAACAGCGGGCTTT	2022
Dy			
Dy	1960	CAGGTTCGACTAACCCGAAGACTTCAAAGCCGACAATCTTCTTGTAACAGCGGGCTTT	2019
Dy			
Dy	2023	TACGCCCGCAGCGGGAGAAATGGCGGTACTATTTTTCAATAATAGATGGGAATCTCTT	2082
Dy			
Dy	2020	TATGCCCGCAGCGGGAGAAATGGCGGTATATATATCGACAGCGACCGGAATTCGGT	2079
Dy			
Dy	2083	GATATACTGAGATACTGAAAATGAAGCTGAAGC	2117
Dy			
Dy	2080	CGGTATTGGGGCGAAGAAAAAGATACAAGGAGGC	2114
Dy			
	RESULT 4		
	AAAX23319		
ID	AAAX23319	standard; cDNA; 2277 BP.	
XX	AAAX23319;		
DT	11-JUN-1999	(first entry)	
XX	N. meningitidis strain BNCV LbpB cDNA.		
DE	LbpB; lactoferrin binding protein; vaccine; neisserial disease;		
XX	meningitis; diagnosis; treatment; ds.		
KW	Neisseria meningitidis.		
OS			
XX	Key Location/Qualifiers		
PH	100..2277		
FT	/*tag= a		
FT	/product= "LbpB"		
XX	WO9909176-A1.		
PN	25-FEB-1999.		
PD			
XX	10-AUG-1998; 98WO-EP005117.		
PF			
XX	15-AUG-1997; 97GB-00017423.		
PR	05-FEB-1998; 98GB-00002544.		
PP			
XX	(UYUT-) RIJUSUNIV UTRECHT.		
PA	(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.		
XX	Pettersson-Fernholm AM, Tommassen JPM;		
PI	WPI; 1999-190165/16.		
DR	P-PSDB; AAW93492.		
XX	New lactoferrin-binding protein B polynucleotides - obtained from		
PT	Neisseria meningitidis, used to develop products for the diagnosis,		
PT	prevention and treatment of neisserial disease, e.g. meningitis.		
XX	Claim 2; Page 74-78; 116pp; English.		
XX	This invention describes novel lactoferrin-binding protein B (lbpB)		
CC	strains of Neisseria meningitidis. The products of this invention can be		
CC	used for vaccinating humans against neisserial disease e.g. meningitis.		
CC	Antibodies raised against the proteins of the invention can be used for		
CC	diagnosing or treating neisserial disease in humans. The lbpB		
CC	polypeptides can also be used for identifying compounds which inhibit the		
XX	polypeptides		
SQ	Sequence 2277 BP; 700 A; 469 C; 573 G; 535 T; 0 U; 0 Other;		
	Query Match 66.9%; Score 1490.2; DB 2; Length 2277;		
	Best Local Similarity 82.7%; Pred. No. 0;		
	Matches 1859; Conservative 0; Mismatches 298; Indels 90; Gaps 10;		
Dy	1 ATGTGTAACCGGAATATGGCGCATGTCTTGTGGCCCTTACTTTTGGCATCTTGATT	60	

Page 1/3

QY	1141	TTGGATTCTCTGAAATTTTCGGTTGACGAGCGACGGATAAAAAATGCCCGCCGTTTGCC	1200
DB	1198	TTGGATTCTCTGAAATTTTCGGTTGATGAGCGAAGTGGTGAATCCCGACCGTTTGCC	1257
QY	1201	ATTTCCTCTGCCCAGATTTTGGCCATCCCGACAAATCTCTTGTGCGAAGCGCGTGAAT	1260
DB	1258	ATTTCCTCTATGCCGATTTTGGTCATCCGACAAATCTCTTGTGCGAAGCGCATGAAT	1317
QY	1261	CTTTTGGTTAGCCAGAGAAACCATCGAGCTCCCGACCGCAGGAAAAATGACGTCCTG	1320
DB	1318	CTTTTGGTTAGCCAGAGAAACCATCGAGCTTCGCAOGCGAGAAAAATGACCGTCAGT	1377
QY	1321	GCTTGTTCGATTTTCTGACCTATGTGAAATCTCGGACGGATAAAAACTGACCCGCCAGCA	1380
DB	1378	GCTTGTTCGACTTTTTCGACCTATGTGAAATCTCGGACGGATAAAAACTGACCCGCCG	1437
QY	1381	AGTAACCAAGGCGGGAAGATAAGGGAAGATGAAGGATACAGCGTGTGGTAACGAC	1440
DB	1438	GCCAAACCGAAGGC-----GCAGGACGAAGGATTCGACATTGATATGTC	1485
QY	1441	GAAGAAGGCACGGAAGATGAAGCGCAGAGAGGCGAAGGAGCGGAGACGAATCGGC	1500
DB	1486	GAAGAAAGC---GAAGACGAATCGGCGATGAAGAAAGGACCGGAGATGACGCCGCA	1542
QY	1501	GATGAAGGAGGAGTTCGGGAGACGAAGCCGCGAAAAACGAAGCGCGAAGAAAGCAAA	1560
DB	1543	GGAGATGAAGGCACGGAAGAGCAAGCCACAGAAACGAAGACGCGGAGAAAGCAAA	1602
QY	1561	GCTCAAGAACTGAAAGAACCGGAAGAAAGATTCGCGCGCAGAAGCGCGTGTGTCTCA	1620
DB	1603	GCTGAAGAACT-----GAAGAAAGATTCGCGCAGAAGGCAAC---GGCAGTTCA	1650
QY	1621	GACGGCATCTGCGCGCTCCGGAAGCTCTTAAAGGCGAGGATATCGACCTTTCTGTAAA	1680
DB	1651	AACGCCATCTGCTGTCCGGAAGCCTTAAAGGCGAGGATATCGACCTTTCTGTAAA	1710
QY	1681	GGTATCGCACGGCGGAAGCGCATTTCCGCAAACTGGAAAGCAGCTATACCGGCAT	1740
DB	1711	GGTATCGCACGGCAGAAACGAATATTCGCAACTGGAGAGCAGCTATACCGGCAT	1770
QY	1741	TGGGAAGCGGTATCAGAAACCCATTCATGGGAACAATCGCGGATAAAAAGCGCA	1800
DB	1771	TGGGAAGCGGTATCAGAAACCCATTCATGGGAACAATCATCGCGATAAAGAAGCGCA	1830
QY	1801	AAAGCAGAAATTCAGCGTTGATTTTCGCGAGAAATCGATTCGGAACGCTGACGAGAAA	1860
DB	1831	AAAGCAGTAATTTACCGTTGATTTTCGCGAAGAAATCGATTCGGAACGCTGACGAGAAA	1890
QY	1861	AACGGTGTACAACTGCTTTCCATATGAAAAACGGCGTGATTTGAGGGCAATGTTTCCAC	1920
DB	1891	AACGGTGTAGAACTGCTTTCCGTTATGGAACCGCGTGATTTGAGGGCAACGGTTTCCAT	1950
QY	1921	GCACAGCGGCACTCGGATTAACCGGCATCAATCTTTTCGGGAATGATTCGACTAATCCT	1980
DB	1951	GCACAGCGGCACTCGGATGACGCGCATCGACCTTTCCGGCAGGGTTGACCAACCG	2010
QY	1981	CCAAGTTTCAAGCCCAATAATCTTCTGTGAAACAGGCGGTTTTCAGGCCCGCAGCGAG	2040
DB	2011	CAGATCTTCAAGCTTAATCAATCTTGTGTAAGGAGGATTTTACGGCCCCGAAGCGGAG	2070
QY	2041	GAATTGGCGGTACTATTTTCAATAATGATGCGAAATCTCTTGGTATAACTGAAGATACT	2100
DB	2071	GAATTGGCGGTATTTATTTTCAATAATGATGCGAAATCTCTTGGTATAACTGAAGTACT	2130
QY	2101	GAAAATGAAGCTGAAGCTGAAGTTGAAATGAAGCTGGTGT-----	2141
DB	2131	GAAAATGAAGTTGAAGCTGATGTGTATGTGTGATGTGTGATGTGTGATGTGTGATGTGTG	2190
QY	2142	--TGGCGAACAGTTTAAACCTCAAGCTAAACCCCAATTTCCGCGTGGTATTCGTTCCGAAG	2199
DB	2191	GATGTTGAACAGTTTAAACCTGAAGTTAAACCCCAATTTCCGCGTGGTATTCGTTCCGAAG	2250

QY 2200 AAAGATAATAAAGAGGTGAAAAATGA 2226  
 |||||  
 Db 2251 AAAGATAATAAAGAGGTGAAAAATGA 2277

RESULT 5  
AAA81489

Continuation (2 of 9) of AA81489 from base 100001 (N. meningitidis partial DNA sequence)  
 WP Sequence split into 9 fragments LOCUS AA81489 Accession AA81489

Query Match	66.4%	Score 1477.2	DB 3	Length 110000;
Best Local Similarity	81.4%	Pred. No. 0;		
Matches 1832; Conservative	0;	Mismatches 358;	Indels 60;	Gaps 8;

63541 TCCTATGAGGCTAGGATGCGACGACGAGGAAAGCATCTCGGATATACGGTTGAT 63482  
 775 TTGATAGAAACCTTTGACGGGTCAATTAATAAATAAGTATGTGCAAAAGAAAC 834  
 63481 TTTGATACAAACCTGATGCGAAGCTGATTAATAATCAGTATGTGCAAAATAAAGT 63422  
 835 GATGAA-----AGAAACCACTGACCAATTTACGACATTAACGCAACATTCGACGCG 885  
 63421 AATCCAAATGAGCCCAAAACCGCTGACCATTTACGACATTTACGCAACATTCGACGCG 63362  
 886 AACCGCTTTACCGGAGTGCACAAAGTTAAACCGAGTTGAAGACGAGCAGCGCTGATAAA 945  
 63361 AACCGCTTTACCGGAGTGCACAAAGTTAGACCGAGTTGAAGACGAGCAGCGCTGATAAA 63302  
 946 GAGCATTTGTTTTTCATPACCGATGCCGATCAGCGCTTTGAGGGGGTTTTTTCGGCGAT 1005  
 63301 GAATATTTGTTTTTCCATACCGATGCCGATCAGCGCTTTGAGGGGGTTTTTTCGGCGAT 63242  
 1006 AAGGGGGAAGACTTTGCGGAGGTTTTATCAGACGACGACGACGAGTATTCGGCGTATTC 1065  
 63241 AACGGAGAAGACTTTGCGGAGGTTTTATCAGACGACGACGAGTATTCGGCGTATTC 63182  
 1066 GCAGGCA---AAAAACCAACGCAATCAACCGCAGACGATACAAATCCTGCTATGCCGTCT 1122  
 63181 GCAGGCAACCAACCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 63122  
 1123 GAAACACACACAAATCTTGATTTCTGAAATTTCTGAAATTTCTGAAATTTCTGAAATTTCT 1182  
 63121 GAAACACACACAAATCTTGATTTCTGAAATTTCTGAAATTTCTGAAATTTCTGAAATTTCT 63062  
 1183 ATGCGCGCGCTTTGCCATTTCCCTCTGCGCGATTTGCGCATTCGCGCAAACTCCTT 1242  
 63061 AATCCCGGTGAGTTTGGCATTTCCCTCTGCGCGATTTGCGCATTCGCGCAAACTCCTT 63002  
 1243 GTGCAAGGCGTGAATTTCTTTGTTAGCCAGAGAAACCATCGAGCTTGCAGCGC 1302  
 63001 GTGCAAGGCGTGAATTTCTTTGTTAGCCAGAGAAACCATCGAGCTTGCAGCGC 62942  
 1303 AGGAAATGACCGTCCGTGCTTTGCGATTTCTGAAATTTCTGAAATTTCTGAAATTTCT 1362  
 62941 AGGAAATGACCGTCCGTGCTTTGCGATTTCTGAAATTTCTGAAATTTCTGAAATTTCT 62882  
 1363 AAACTGACCGCCGACGATTAACCAAGCGGAGATTAAGGGAGGATGAAGAGGAT 1422  
 62881 CAAACGGAACGTCGCGCGCCGACCAAGCGGAGGATTAAGGGAGGATGAAGAGGAT 62822  
 1423 ACAGGCGTTGTTAAACGAGAAAGGACGAGATGAAGCCGAGAGGACGAGCGAAGGA 1482  
 62821 ACAGGCGTTGTTAAACGAGAAAGGACGAGATGAAGCCGAGAGGACGAGCGAAGGA 62768  
 1483 GCGAAGACGAAATCGCGGATTAAGGAGGAGTGCAGGAGACGAGAGCGCGAGAAACGAA 1542  
 62767 ACCGAGACGCGACCGCTTAAAGACGAGGACGAGAGGACGAGAGCGCGAGAGGATGA 62708  
 1543 GCGCGGAGAGACGAGACGAGCTGAGACCTGAGAACCCGAGAGGATTCGCGGAGAA 1602  
 62707 -----GATGAGCTGAGAAACCCGAGAGGATTCGCGGAGAA 62669  
 1603 GCGCGGAGGTTGTTGATGAGCGGATTCGCGGATTCGCGGATTCGCGGATTCGCGGATTC 1662  
 62668 GAAGCGGACGCGGTTGAGCGGATTCGCGGATTCGCGGATTCGCGGATTCGCGGATTC 62609  
 1663 ATGACCTTTTCTGAAAGTATTCGCGGAGGATTCGCGGATTCGCGGATTCGCGGATTC 1722  
 62608 ATGACCTTTTCTGAAAGTATTCGCGGAGGATTCGCGGATTCGCGGATTCGCGGATTC 62549  
 1723 GCAGCTATACCGGCTTTCGGAAGCGGATTCGAGAAACCCGATTCGAGGACGATTCAT 1782  
 62548 GCACACTATACCGGCTTTCGGAAGCGGATTCGAGAAACCCGATTCGAGGACGATTCAT 62489  
 1783 GCGGATACAAAGCGGCAAGGATTTGAGCTTTCGCGGAGGATTCGCGGAGGATTCGCGGATTC 1842

62488 GCGGATACAAAGCGGCAAAAGCAGTATTTACCTGATTTCCGCAAGAAATCGATTTCC 62429  
 1843 GGAACGCTGACGAGGAAACCGGTGTACAACTGCTTTCCATATTTGAAACCGGCTGATT 1902  
 62428 GGAACGCTGACGAGGAAACCGGTGTAGAACCTGCTTTCCATATTTGAAACCGCAAGATT 62369  
 1903 GAGGCAATGTTTCCACGCGACAGCGCTCGGATTAACCGGATCAATCTTTTCGGGA 1962  
 62368 GAGGCAATGTTTCCACGCGACAGCGCTCGGATTAACCGGATCAATCTTTTCGGGA 62309  
 1963 AATGATTCGATTAATCTCCAAAGTTTCAAGCCATTAATCTTTGTAACAGGCGCTTT 2022  
 62308 AATGTTTCGACCGCCCAAAACCTTCAAGCTAGTAACTTTCTGTAAGAGGGGATTT 62249  
 2023 TACGCGCGCAGCGGAGGAAATTCGGCGGTACTATTTTCAATATGATGGGAAATCTCTT 2082  
 62248 TACGCGCGCAGCGGAGGAAATTCGGCGGTACTATTTTCAATATGATGGGAAATCTCTT 62189  
 2083 GGTATACTGAAGATACCTGAAAA-----TGAAGCTGAAGCTGAAGTTGAAATGAAGCT 2136  
 62188 GGTATACTGAAGATACCTGAAAA-----TGAAGCTGAAGCTGAAGTTGAAATGAAGCT 62129  
 2137 GGTGTTGCGGACAGCTTAAACCTGAAGCTAAACCCCAATTCGGCGTGTATTCGGTGG 2196  
 62128 GATGTTGCAACAGCTTAGAATCTGAAGTTAAACCAATTCGGCGTGTATTCGGTGG 62069  
 2197 AAGAAAGATTAATAAGAGCTGGAATAATGA 2226  
 62068 AAGAAAGATTAATAAGAGCTGGAATAATGA 62039

RESULT 6  
 AAF21611/c  
 ID AAF21611 standard; DNA; 349980 BP.  
 XX AAF21611;  
 AC AAF21611;  
 DT 13-MAR-2001 (first entry)  
 XX Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.  
 DE Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;  
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;  
 KW ds.  
 OS Neisseria meningitidis.  
 XX WO200066791-A1.  
 PN 09-NOV-2000.  
 XX 08-MAR-2000; 2000WO-US005928.  
 PF 30-APR-1999; 99US-0132068P.  
 PR 08-OCT-1999; 99WO-US02573.  
 PR 28-FEB-2000; 2000GB-09004695.  
 XX (CHIR) CHIRON CORP.  
 PA (GENO) INST GENOMIC RES.  
 XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;  
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
 PI Rappuoli R, Frazer CM, Grandi G;  
 XX WPI; 2000-647603/62.  
 DR Neisseria meningitidis B full length genome sequence and open reading  
 PT frames are used to detect, treat and prevent Neisserial infections.  
 XX Claim 7; Appendix A; 692pp; English.  
 CC The present invention describes the full length genome of Neisseria  
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613





QY 1783 GCGGATAAAAGCGGCAAAACGAGAAATTTGACGTTGATTTCCGGCGAGAAATCGATTCC 1842  
DB |||||||  
QY 97717 GCGGATAAAAGCGGCAAAACGAGAAATTTGACGTTGATTTCCGGCGAGAAATCGATTCC 97658  
DB |||||||  
QY 1843 GGAACGCTGACGGAGAAAACGGTGTACAACCTGCTTTCCATATTGAAAACGGCGTGATT 1902  
DB |||||||  
QY 97657 GGAACGCTGACGGAGAAAACGGTGTAGAACCTGCTTTCCATATTGAAAACGGCAAGATT 97598  
DB |||||||  
QY 1903 GAGGCAATGTTTCCACGCGACAGCGGCACTCGGGATACGGCATCAATCTTTCGGGA 1962  
DB |||||||  
QY 97597 GAGGCAACGGTTTCTACGCGACAGCAGCACTCGGGAGAACGGCATCAATCTTTCGGGA 97538  
DB |||||||  
QY 1963 AATGATTCGACTAACTCCCAAGTTTCAAGCCAAATAATCTTCTTGTAAACGGCGCTTT 2022  
DB |||||||  
QY 97537 AATGTTGACCGACCCCAAACTTCCAAAGCTAGTAATCTTCTGTTAGAACGGGATTT 97478  
DB |||||||  
QY 2023 TACGGCCCGCAGCGGAGGAATTTGGCGGTACTATTTTCAATAATGATGGGAAATCTCTT 2082  
DB |||||||  
QY 97477 TACGGCCCGCAGCGGAGGAATTTGGCGGTACTATTTTCAATAATGATGGGAAATCTCTT 97418  
DB |||||||  
QY 2083 GGTATACTGAAGATACTGAAA-----TGAAGCTGAAGCTGAAGTTGAAAATGAAGCT 2136  
DB |||||||  
QY 97417 GGTATACTGAAGATACTGAAAATAAAGTTGATTTGAAGCTGAAGTTGATGCTGAAGTT 97356  
DB |||||||  
QY 2137 GGTGTTGGGAAACAGTTAAACCTGAAGCTAAACCCCAATTCGGGCTGTTATTCGGTGCG 2196  
DB |||||||  
QY 97357 GATGTTGGCAACAGTTAGAACTGAACTTGAAGTTAAACCAATTCGGGCTGTTATTCGGTGCG 97298  
DB |||||||  
QY 2197 AAGAAAGATAATAAGAGAGGTGGAATAATGA 2226  
DB |||||||  
QY 97297 AAGAAAGATAATGAGAGGTGGAATAATGA 97268  
DB |||||||

RESULT 7  
AA23322  
ID AA23322 standard; cdna; 2262 BP.  
XX  
AC AA23322;  
XX  
DT 11-JUN-1999 (first entry)  
XX  
DE N. meningitidis strain M990 LbpB cdna.  
XX  
KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;  
KW meningitis; diagnosis; treatment; ds.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT 1. .2262  
FT /\*tag= a  
FT /product= "LbpB"  
XX  
PN W0909176-A1.  
XX  
XX 25-FEB-1999.  
XX  
PF 10-AUG-1998; 98WO-EP005117.  
XX  
XX 15-AUG-1997; 97GB-00017423.  
PR 05-FEB-1998; 98GB-00002544.  
XX  
XX (UUT-) RIJKSUNIV UTRECHT.  
PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.  
XX  
PI Pettersson-Fernholm AM, Tommassen JPM;  
XX  
XX WPI; 1999-190165/16.  
DR  
DR P-PSDB; AAW93495.  
XX  
XX New lactoferrin-binding protein B polynucleotides - obtained from  
PT Neisseria meningitidis, used to develop products for the diagnosis,  
PT prevention and treatment of neisserial disease, e.g. meningitis.

XX  
PS  
XX  
CC This invention describes novel lactoferrin-binding protein B (LbpB)  
CC strains of Neisseria meningitidis. The products of this invention can be  
CC used for vaccinating humans against neisserial disease e.g. meningitis.  
CC Antibodies raised against the proteins of the invention can be used for  
CC diagnosing or treating neisserial disease in humans. The LbpB  
CC polypeptides can also be used for identifying compounds which inhibit the  
CC polypeptides  
XX  
SQ Sequence 2262 BP; 698 A; 487 C; 590 G; 487 T; 0 U; 0 Other;  
Query Match 64.8%; Score 1442.2; DB 2; Length 2262;  
Best Local Similarity 80.3%; Pred. No. 0;  
Matches 1828; Conservative 0; Mismatches 383; Indels 66; Gaps 9;  
QY 1 ATGTGTAACCAACCAATTTATGGCGCAATTTGTTGGCTTACTTTTGGCATCTTTGATT 60  
DB |||||||  
QY 61 GCGCGCAATTTGCGGTCGCGCTGTTGTCGAATCAACGCGACCGCG----- 108  
DB |||||||  
QY 61 GCGCGCAATTTGCGGTCGCGCTGTTGTCGAATCAACGCGACCGCGCAACTCTGTCA 120  
DB |||||||  
QY 109 TACCCCGTCACCTTCAAGTCTAAGGACGTTCCCACTCCGCCCCCTGCCAAACCTTCTATA 168  
DB |||||||  
QY 121 GATTCCAATCTTCAATCTCTCGGTAAGCTGCTCCAGCTCTCTGCCGAGCTTCGGTA 180  
DB |||||||  
QY 169 GAAACACGCGGTCGCGCTCAACCGGCGCTGCGGTCGCGGCAATGGGCTGTTGAGG 228  
DB |||||||  
QY 181 GAAATCAGCCCGT-----CAAAGCGCGCGCGCTGCGGTCGCGCAATGGGCTGCCAAG 234  
DB |||||||  
QY 229 CGGATTTTCGCAACTTCTGATBAAGTTGGCAATGATTTTCCAAATAGCAAAACAAGCAGAA 288  
DB |||||||  
QY 235 CGGAATATCGCAACTTTTGATAAAATGTAATGAAATTTCCCAATGTAAGCAGGACAG 294  
DB |||||||  
QY 289 GAAAAGCTGCTCGTTTAAAGAGGTGATGTTCTGTTTATACGGTTTCAAAAAGATAAA 348  
DB |||||||  
QY 295 GAGTATCTGCCCTCAAGAGAGGATATCTGTTTATAGACGGTACCGGAAAGAACAG 354  
DB |||||||  
QY 349 CTTCAAGTGGCTTAAGATAAAATTCATCAACGCAATCTTAATGTAGAAATTAGGACATCA 408  
DB |||||||  
QY 355 GCTGCAAACTTTAAAAAGGAAATCAACGAGCGCATCTTAATGCAACCAATCTACAGTCC 414  
DB |||||||  
QY 409 GAAATGAAATTAATAAATATGTTATGATGATGCGGTCGCGTATGATATATATA 468  
DB |||||||  
QY 415 GATTTAAAGATGATGCGTATCAATAAATATGTCGGGCGGATGATGTTATATAGTA 474  
DB |||||||  
QY 469 AACGGAACAGATGAAATTCAGTGGACTTCAAAATCGCAAGCAGTTTCTAATCGTTTGGC 528  
DB |||||||  
QY 475 TATGGAACAGATGAAATCGAAGCAACTCAGCGGTTAGCGGTTACCCACCGCTTAGGT 534  
DB |||||||  
QY 529 TACGAGGTTTGTATATTTATTCGCGAGAAATCTTCCCAATCTTACCGAGCGGGA 588  
DB |||||||  
QY 535 TATGAGGTTTGTATATTTATTCGCGAGAAACGTCCTTCCCAATCTTACCGAGTGGGGA 594  
DB |||||||  
QY 589 ACGGTCAATATTCGCGTAATTCGGCAATATATGACCGATGCCATACGTCTATCGAACAGGA 648  
DB |||||||  
QY 595 ACGGTGAATATTTCTGGTAATTCGGCAATATATGACCGATGCCAAGCTCATCGAGCAGGT 654  
DB |||||||  
QY 649 AAAGCAGGAGATCTTAGCGAAGATTTGGGTTATCTCGTTTATTTACCGTCAAAATGTCGGA 708  
DB |||||||  
QY 655 CAGGC--GTTGGCATTGCAATTTGGGTTATATCAATTTTATGTAACGATGTTGTT 711  
DB |||||||  
QY 709 GCAACTTCTATGCTCGGACTCCGAGCGCGGAGGAAACATCTCTCCGATATACG 768  
DB |||||||  
QY 712 GCAACTTCTATGCGGCTAAGGATGTCGACGAAAGGAAAGCATCTCTGCAATATACG 771  
DB |||||||  
QY 769 GTTGATTTTCGATAAGAAACCTTTGACGGGTCAATTAATTAATAATCAGTATGTGCAAAAG 828  
DB |||||||  
QY 772 GTTGATTTTGAATAACAAACCATGATGCAAGCTGATTAATAATCAGTATGTGCGAAT 831  
DB |||||||





[illegible]

2032 AAAGCCAGTAATCTTCTCTAGAGGAGGATTTTATGTTCCGACGGCGCAGAGTTGGGT 2091  
 2050 GGTAATATTTCAATAATGATGGGAAA 2076  
 2092 GGTAATATTTCAATAATGATGGGAAA 2118

RESULT 9

AAA81482/c

ID AAA81482 standard; DNA; 14652 BP.

AC XX

AT XX

CT XX

DT 04-DEC-2000 (first entry)

DE XX

N. meningitidis partial DNA sequence gnm\_30 SEQ ID NO:30.

KW XX

Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;

KW XX

antigen; vaccine; diagnosis; infection; antibacterial; identification;

KW XX

Meningococcus B; MenB; ds.

OS XX

Neisseria meningitidis.

XX XX

WO200022430-A2.

PN XX

20-APR-2000.

XX XX

08-OCT-1999; 99WO-US023573.

PF XX

09-OCT-1998; 98US-0103794P.

PR XX

30-APR-1999; 99US-0132068P.

XX XX

(CHIR ) CHIRON CORP.

PA XX

Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;

PI XX

Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;

PI XX

Rappuoli R, Pizza M;

XX XX

WPI; 2000-318079/27.

DR XX

Isolated nucleotide sequences of Neisseria meningitidis which can be used

PT XX

in the diagnosis and treatment of N. meningitidis infection and other

PT XX

Neisserial infections, for example, N.gonorrhoea.

PT XX

Claim 7; Page 582-586; 1760pp; English.

PS XX

The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions

XX XX

Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;

Query Match 48.4%; Score 1077.6; DB 3; Length 14652;  
 Best Local Similarity 84.1%; Pred. No. 1.5e-260;  
 Matches 1292; Conservative 0; Mismatches 199; Indels 45; Gaps 5;

QY	709	GCAACTTCTTATGTCGCACTGCCGACGACCGGGGAGGAAAACATCTCTGCGCAATATACG	768
DB	14652	GCAACTTCTTATGAGGCTAGGATGCCGACGACGGGAAAACATCTCTGCGCAATATACG	14593
QY	769	GTTGATTTTCGATAAGAAAACCTTTGACGGCTCAATTAATTAATAATCAGTATGTGAAAAG	828
DB	14592	GTTGATTTTCGATAAGAAAACCTTTGATGCGAGCTGATTAATAATCAGTATGTGAAAAT	14533
QY	829	AAAACCGGATGAA-----AAGAAACCACTGACCACTTTACGACATTTACCGCAACATTTG	879
DB	14532	AAAAGTATCCAAATGAGCCCAAAAACCGCTGACCACTTTACGACATTTACCGCAACATTTG	14473
QY	880	GACGGCAACCGCTTTACCGGAGTCCCAAGGTTAAACCGAGTTGAAGACGAGCCACGCT	939
DB	14472	GACGGCAACCGCTTTACCGGAGTCCCAAGGTTAAACCGAGTTGAAGACGAGCCACGCT	14413
QY	940	GATAAAGAGCATTTGTTTTTCCATACCGATCCGATCAGCGCTTTGAGGGCGGTTTTTTC	999
DB	14412	GATAAAGATATTTGTTTTTCCATACCGATCCGATCAGCGCTTTGAGGGCGGTTTTTTC	14353
QY	1000	GGCGATAAGGGGAGAGCTTTGCCGAGCGTTTATCAGCAACGACAAACAGCGTATTCGGC	1059
DB	14352	GGCGATAACGGAGAGAGCTTTGCCGAGCGTTTATCAGCAACGACAAACAGCGTATTCGGC	14293
QY	1060	GTATTCGCGGCA---AAAAAACAACGATCAACGAGCAGATACAAATCTCTGCTATG	1116
DB	14292	GTATTCGCGGCAACCAAAAACAAGAGACGAGCAAAAACGAGCAGATACAAACCTTGCCCTG	14233
QY	1117	CCGCTCTGAAAAACACACCAAAATCTTGATTTCTGAAAAATTTCCGTTGAGGCGCGACG	1176
DB	14232	TCGCTCTGAAAAACAACCAAAATCTTGATTTCTGAAAAATTTCCGTTGAGGCGCGACG	14173
QY	1177	GATAAAATGCCCGCCCGTTTGCCATTTCCCTCTGCCCGATTTTGGCCATCTCCGACAAA	1236
DB	14172	GATAAAATGCCCGCGAGTTTGCCATTTCCCTCTATGCCCGATTTTGGTCATCCGACAAA	14113
QY	1237	CTCCTTTGCGAGGGCGTGAATTTCTTTGGTTAGCAAGAGAAAACCATCGAGCTTGCC	1296
DB	14112	CTCCTTTGCGAGGGCGTGAATTTCTTTGGTTAGCAAGAGAAAACCATCGAGCTTGCC	14053
QY	1297	GACGGCAGGAAAATGACCGTCCGTCGTTGTTGGCAATTTCTGACCTATGTGAAACTCGGA	1356
DB	14052	GATGTTAGGAAAACGACAAATCCGNAACCTGCTGCGATTTTCTGACCTATGTGAAACTCGGA	13993
QY	1357	CGGATAAAAACCTGACCCGCCCAAGTAACCAAGGCGGAGAGATAAAGGGAAGGATGAA	1416
DB	13992	CGGATGCAAAACCGAAACGTCGCCGCCCAACCGAAGGCGGAGGACGAGAGGAGCGAA	13933
QY	1417	GAGGATACGCGCTTGTTAAGCAGCAAGAGGACGGAAGTGAAGCCGCGAGAGGAGCAGC	1476
DB	13932	GAGGATACGCGCTTGTTAAGCAGCAAGAGGACGGAAGTGAAGCCGCGAGAGGAGCAGC	13879
QY	1477	GAAGGAGCGCAAGACGAAATCGGCGATGAAGGAGGAGGTCGGGAAGACGAGCGCAGAA	1536
DB	13878	GAAGGACCGGAGACGCGCGCTTAAGACGAGAGGAGCGGAAGACGAGCGCTAGAA	13819
QY	1537	AACGAAGGCGCGGAGGAGGACGAAAGCTGAAGAACCTCGAAGAACCCGGAAGGATCCCG	1596
DB	13818	GGTGAA-----GATGAAGCTGAAGAACCCGGAAGGATCCCG	13780
QY	1597	GCAGAGCGCGCGTGGTGGTTGACAGCGGATCTGCGCCGCTCGGAGCTCTTAAAGGC	1656
DB	13779	ACGAAGAGCGCGGACGCGGTTTACAGCGGATCTGCGCCGCTCGGAGGAGCCCTTAAAGGC	13720
QY	1657	AGGATATCGACCTTTTCTTGAAGGATATCGGACGCGGAGGAGCGGATTTCCGCAACT	1716
DB	13719	AGGATATCGACCTTTTCTTGAAGGATATCGGACGCGGAGGAGCGGATTTCCGCAACT	13660

QY 1717 GGAAGACGCTATACCGGCACTTGGGAAGCGGTATCAGCAAAACCCATTCAATGGAC 1776  
 Db |||||  
 QY 13659 GGAGAGCAGACTATACCGGCACTTGGGAAGCGGTATCGGCAAAACCCATTCAATGGAC 13600  
 Db |||||  
 QY 1777 AATCATGCGGATAAAAAAGCGCAAAAGCAGAAATTTGAGTTTTCGGGAGAAATCG 1836  
 Db |||||  
 QY 13599 AATCAGGCGGATAAAGAGCGCAAAAGCAGTAATTTACGTTGATTTTCGGCAAGAAATCG 13540  
 Db |||||  
 QY 1837 ATTTCGGAAACGCTGACGAGAAACCGGTAGCAACCTGCTTTCATATTGAAACCGC 1896  
 Db |||||  
 QY 13539 ATTTCCGGAACGCTGACGAGGAAACCGGTAGCAACCTGCTTTCATATTGAAACCGC 13480  
 Db |||||  
 QY 1897 GTGATTGAGGCAATGCTTTCACCGGACAGCGGCACTCGGATAACGGCATCAATCTT 1956  
 Db |||||  
 QY 13479 AAGATTGAGGCAACGCTTTCACCGGACAGCGGCACTCGGATAACGGCATCAATCTT 13420  
 Db |||||  
 QY 1957 TCGGGAATGATTCGACTTAATCTCTCAAGTTTCAAGGCAATAATCTTCTGTAAACGCG 2016  
 Db |||||  
 QY 13419 TCGGGAATGCTTTCACCGGACAGCGGCACTCGGATAACGGCATCAATCTTCTGTAAACGCG 13360  
 Db |||||  
 QY 2017 GGCTTTTACGCGCGGCGGAGGAAATGGCGGTACTATTTTCAATAATGATGGGAA 2076  
 Db |||||  
 QY 13359 GGAATTTACGCGCGGCGGAGGAAATGGCGGTATTTTCAATAATGATGGGAA 13300  
 Db |||||  
 QY 2077 TCTCTTGTATAACTGAAGACTACTGAAAA-----TGAAGCTGAAGCTGAAGTTGAAAAAT 2130  
 Db |||||  
 QY 13299 TCTCTTGTATAACTGAAGGTAAGTGAATAAAGTTGATTTGAAGCTGAAGTTGATGCT 13240  
 Db |||||  
 QY 2131 GAAGCTGTGTGGCGAAGCAGTTAAACCTGAAGCTAAACCCCAATTCGGCGTGTATTC 2190  
 Db |||||  
 QY 13239 GAAATTGATGTTGGCAACAGTTAGAAATCTGAAGTTAAACCAATTCGGCGTGTATTC 13180  
 Db |||||  
 QY 2191 GGTGCGAAGAAAGATAATAAGAGCTGGAATAATCA 2226  
 Db |||||  
 QY 13179 GGTGCGAAGAAAGATAATGAGAGCTGGAATAATCA 13144  
 Db |||||  
 RESULT 10  
 ID AAF91389 standard; DNA; 1000 BP.  
 AC AAF91389;  
 XX AAF91389;  
 DT 04-MAY-2001 (first entry)  
 XX  
 DE N. meningitidis (serogroup B) LbpA gene upstream sequence, SEQ ID:15.  
 XX  
 KW Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine;  
 KW genetically modified; protective antigen expression; LPS detoxification;  
 KW LPS; lipid A; homologous recombination vector; immunisation;  
 KW immunoprotective; non-toxic; paediatric; cyclic; circular; ds.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 FN WO200109350-A2.  
 XX  
 PD 08-FEB-2001.  
 XX  
 PF 31-JUL-2000; 2000WO-EP007424.  
 XX  
 PR 03-AUG-1999; 99GB-00018319.  
 XX  
 XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Berthet FJ, Dalemans WLJ, Denoel P, Dequesne G, Feron C, Lobet Y;  
 PI Poolman J, Thiry G, Thomnard J, Voet P;  
 XX  
 DR WPI; 2001-138654/14.  
 XX  
 PT New isolated polynucleotide useful for outer membrane vesicle preparation  
 PT from Gram-negative bacterial strain for vaccination of microbial  
 PT infections.  
 XX

PS Claim 46; Page 81; 128pp; English.  
 XX  
 CC The invention relates to a genetically-engineered outer membrane vesicle  
 CC (bleb) preparation from a Gram-negative bacterium for use as a vaccine.  
 CC The blebs of the invention are improved with respect to their  
 CC immunogenicity and toxicity by the introduction of one or more genetic  
 CC changes to the chromosome of the bacterium from which the blebs are  
 CC derived. The changes made include the upregulation of protective antigen  
 CC expression, the downregulation of immunodominant non-protective antigen  
 CC expression, and genetic changes which result in detoxification of the  
 CC Lipid A moiety of lipopolysaccharide (LPS). The invention also  
 CC encompasses modified Gram-negative bacterial strains from which the bleb  
 CC preparations are made, a vector suitable for performing recombination  
 CC events (for the generation of the modified bacterial strains),  
 CC bacterially-derived nucleic acid sequences used in such a vector, and an  
 CC immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole  
 CC cell vaccine suitable for paediatric use. The bleb preparation is useful  
 CC in the manufacture of a medicament for immunising a human host against a  
 CC disease caused by infection of one or more of the following: *Neisseria*  
 CC meningitidis, *Neisseria gonorrhoeae*, *Haemophilus influenzae*, *Moraxella*  
 CC catarrhalis, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, and *Chlamydia*  
 CC pneumoniae. The invention may also be used to provide immunisation against  
 CC the influenza virus. Bacterially derived nucleotide sequences of the  
 CC invention are used in the performance of homologous recombination events  
 CC up to 1000 bp upstream of a bacterial chromosomal gene in order to either  
 CC increase or decrease expression of that gene. Immunoprotective and non-  
 CC toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more  
 CC immunogenic, less toxic and safer, and are particularly useful for  
 CC paediatric use. The present sequence represents a specifically claimed  
 CC *Neisseria meningitidis* nucleic acid sequence  
 XX  
 SQ Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;  
 Query Match 32.2%; Score 716; DB 4; Length 1000;  
 Best Local Similarity 84.6%; Pred. No. 5.8e-170;  
 Matches 865; Conservative 0; Mismatches 120; Indels 37; Gaps 4;  
 QY 1216 GATTTTGGCCATCCCGACAAACTCTCTGTCGAAGGCGCTGAAATTCCTTTGTTAGCCAA 1275  
 Db 1 GATTTTGGTCATCCCGACAAAGCTTCTTGTGCAAGGCGCTGAAATTCCTTTGTTAGCCAA 60  
 QY 1276 GAGAAACCATCGAGCTTTCGACGCGGAGAAATGACCGCTCGTGTGTTGCGATTTT 1335  
 Db 61 GAGAAACCATCAAGCTTTCGCGATGCGCAGGGAATGACCGTCCGTGTTGTCGACTTT 120  
 QY 1336 CTGACCTATGTGAACTCGGAGGATGAAAGGATACAGCGCTTGGTAAACGCAAGGACGCGAA 1455  
 Db 121 TTGACCTATGTGAAACTCGGAGGATGAAAGGATGAAAGGATGAAAGGATGAAAGGATGAAAGG 180  
 QY 1396 GAAAGATAAGGGAAGGATGAAAGGATGAAAGGATGAAAGGATGAAAGGATGAAAGGATGAAAGG 240  
 Db 181 GAAGATAAGGGAAGGATGAAAGGATGAAAGGATGAAAGGATGAAAGGATGAAAGGATGAAAGG 240  
 QY 1456 GATGAAGCGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1515  
 Db 241 GAAAGTTTCCGAAGATGAAAGGCGGAGAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 279  
 QY 1516 GCGGAAGACGAGCGCGAGAGAAACGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1575  
 Db 280 GTCGAAG 339  
 QY 1576 GAAACCGGAAG 1635  
 Db 340 GAAACCGGAAG 399  
 QY 1636 GCTCCGGAAGCTCTTAAAGGAGGAGGATATCGACCTTTTCTTCTGAAAGGATATCGCAGCGG 1695  
 Db 400 GCCTCGGAAGCTCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 459  
 QY 1696 GAAAGCGGACATTCGCAAACTGGAAG 1755  
 Db 460 GAAAGCGGACATTCGCAAACTGGAAG 519







Db 652 GTTATACCACATATTATGATGTAATGAAATGGGCAACTCTTATGAGGCTA 702

RESULT 13

ABS67377

ID ABS67377 standard; DNA; 3300 BP.

XX AC ABS67377;

XX DT 29-NOV-2002 (first entry)

XX DE Neisseria gonorrhoeae lbpA gene.

XX KW Gram-negative bacterial bleb; PorB; outer membrane protein;

XX KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;

XX KW protective antigen; antibacterial; vaccine; gene; ds.

XX OS Neisseria gonorrhoeae.

XX PN WO200262380-A2.

XX PD 15-AUG-2002.

XX PF 08-FEB-2002; 2002WO-EP001356.

XX PR 08-FEB-2001; 2001GB-00003169.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;

XX DR WPI; 2002-657510/70.

XX DR P-PSDB; ABG31056.

XX PT Novel gram-negative bacterial bleb presenting on its surface PorB outer

XX PT membrane protein from Chlamydia trachomatis or protective antigen from

XX PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.

XX PS Disclosure; Page 48-49; 75pp; English.

XX CC The present invention relates to a new gram-negative bacterial bleb

XX CC presenting on its surface the PorB outer membrane protein from Chlamydia

XX CC trachomatis, or a protective antigen from C. pneumoniae. The invention is

XX CC useful for preventing C. trachomatis or C. pneumoniae infection in a

XX CC host. The present nucleic acid sequence represents a Neisseria

XX CC gonorrhoeae gene as described in the invention

XX SQ Sequence 3300 BP; 897 A; 807 C; 921 G; 675 T; 0 U; 0 Other;

Query Match 10.8%; Score 239.8; DB 6; Length 3300;

Best Local Similarity 91.8%; Pred. No. 1.1e-49;

Matches 269; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 1934 CTCGGGTAACGGCATCAATCTTTCGGGAATGATTCGACTAATCCTCCAGTTTCAAAG 1993

DB 1 CTCGGTAACGGCATCAATCTTTCGGGAATGATTCGACTAATCCTCCAGTTTCAAAG 60

QY 1994 CCAATAATCTTCTTTAAACAGCGGCTTTTACGGCCGCGAGGAGAAATGGCGGTA 2053

DB 61 CCGCAATCTTCTTTAAACAGCGGCTTTTACGGCCGCGAGGAGAAATGGCGGCA 120

QY 2054 CTATTTTCAATATGATGGGAAATCTCTTGTTGTAATCTGAAGATCTGAAATGAAGCTG 2113

DB 121 CTATTTTCAATATGATGGGAAATCTCTTGTTGTAATCTGAAGATCTGAAATGAAGCTG 172

QY 2114 AAGCTGAAGTTGAAATGAAGCTGGTCTTTCGGCAACAGTTAAACCTGAAGCTTAACCCC 2173

DB 173 ----TGAAGTTGAAATGAAGCTGATGTTGGCAACACAGTTAGAACCTTAAACCCC 228

QY 2174 AATTCCGGCGTGGTATTCCGTTCCGAAGAAGATAATAAGAGGTGCGAAATGA 2226

DB 229 AATTCCGGCGTGGTATTCCGTTCCGAAGAAGATAATAAGAGGTGCGAAATGA 281

RESULT 14

AAS90909

ID AAS90909 standard; cDNA; 379 BP.

XX AC AAS90909;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #26713.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG26722.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity.

XX PS Claim 1; SEQ ID NO 26713; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

XX CC sequences. (I) is useful as hybridisation probes, polymerase chain

XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

XX CC and in recombinant production of (II). The polynucleotides are also used

XX CC in diagnostics as expressed sequence tags for identifying expressed

XX CC genes. (I) is useful in gene therapy techniques to restore normal

XX CC activity of (II) or to treat disease states involving (II). (II) is

XX CC useful for generating antibodies against it, detecting or quantitating a

XX CC polypeptide in tissue, as molecular weight markers and as a food

XX CC supplement. (II) and its binding partners are useful in medical imaging

XX CC of sites expressing (II). (I) and (II) are useful for treating disorders

XX CC involving aberrant protein expression or biological activity. The

XX CC polypeptide and polynucleotide sequences have applications in

XX CC diagnostics, forensics, gene mapping, identification of mutations

XX CC responsible for genetic disorders or other traits to assess biodiversity

XX CC and to produce other types of data and products dependent on DNA and

XX CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic

XX CC coding sequences of the invention. Note: The sequence data for this

XX CC patent did not appear in the printed specification, but was obtained in

XX CC electronic format directly from WIPO at

XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 379 BP; 207 A; 25 C; 118 G; 29 T; 0 U; 0 Other;

Query Match 4.1%; Score 91.2; DB 5; Length 379;

Best Local Similarity 59.8%; Pred. No. 1.1e-12;

Matches 153; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 1348 AAATCTCGACCGTAAATAAACTGACCCGACGAAAGTAAACCAAGCGGAGATAAGGG 1407

DB 105 AAACAAAACAAAGACAGAGATATAAGAGAGAGAGAGAGAGAGAGAGAGAA 164

QY 1408 AAGGTGAAGAGGATACAGCGCTTGTGTAACGACGAAGAGCGGAGAGTAAGCGCA 1467



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 12:38:10 ; Search time 161.734 Seconds  
(without alignments)  
7637.968 Million cell updates/sec

Title: US-10-735-098-5  
Perfect score: 2226  
Sequence: 1 atgtgttaaccgaattatgg.....ataagaggtggaataatga 2226

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
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2: /cgn2\_6/ptodata/2/ina/5B-COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A-COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B-COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS-COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
C 1	89	4.0	7218	1	US-08-232-463-14
C 2	75	3.4	929	4	US-09-671-317-14
C 3	75	3.4	1001	4	US-09-671-317-439
C 4	72.6	3.3	2230	3	US-08-448-194-7
5	72.6	3.3	2230	4	US-08-867-921-7
6	72.2	3.2	43795	3	US-08-742-185-101
C 7	69.8	3.1	16442	3	US-08-781-891-208
C 8	69.8	3.1	16442	3	US-09-618-166-208
9	68.2	3.1	1276	3	US-09-177-325-2
10	68.2	3.1	1276	3	US-09-411-812A-2
11	68.2	3.1	1276	4	US-09-590-113-2
12	66.8	3.0	390	3	US-09-197-649-7
13	65	2.9	3211	2	US-08-574-959A-8
14	65	2.9	3211	3	US-09-357-014-8
15	65	2.9	3901	2	US-08-574-959A-6
16	65	2.9	3901	3	US-09-357-014-6
17	64.6	2.9	3489	2	US-08-728-323A-1
18	64.6	2.9	3489	4	US-09-298-568-1
19	64.6	2.9	3489	4	US-09-410-399-1
C 20	64.6	2.9	32207	2	US-08-770-379-20
C 21	64.6	2.9	32207	3	US-08-757-669A-20
C 22	64.6	2.9	32207	4	US-09-230-371A-20
C 23	64	2.9	51259	3	US-08-781-891-209
C 24	64	2.9	51259	4	US-09-618-166-209
25	63.6	2.9	2139	4	US-09-059-584-50
26	62.6	2.8	2696	1	US-07-961-522-1
27	62.6	2.8	2696	1	US-08-217-438-1

28	62.6	2.8	2696	1	US-08-321-978-1	Sequence 1, Appli
29	62.6	2.8	2696	2	US-08-710-584-1	Sequence 1, Appli
30	60.4	2.7	478	4	US-09-621-976-10407	Sequence 10407, A
31	60.4	2.7	1280	4	US-09-220-132-155	Sequence 155, App
C 32	60.4	2.7	1926	4	US-09-249-585A-4	Sequence 4, Appli
C 33	60.4	2.7	1931	4	US-09-130-114-2	Sequence 2, Appli
34	59.6	2.7	125157	4	US-09-913-514-2	Sequence 2, Appli
35	58.8	2.6	696	3	US-09-461-697-193	Sequence 193, App
36	58.8	2.6	699	3	US-09-461-697-191	Sequence 191, App
37	58.8	2.6	717	3	US-09-461-697-189	Sequence 189, App
38	58.8	2.6	774	3	US-09-461-697-187	Sequence 187, App
39	58.8	2.6	819	3	US-09-461-697-185	Sequence 185, App
40	58.8	2.6	1669	4	US-09-461-697-184	Sequence 2, Appli
41	58	2.6	1926	4	US-09-249-585A-2	Sequence 2, Appli
42	58	2.6	1926	4	US-09-410-399-3	Sequence 3, Appli
43	58	2.6	2580	3	US-09-050-863-2	Sequence 2, Appli
44	58	2.6	2580	4	US-09-359-081-2	Sequence 2, Appli
C 45	58	2.6	5452	2	US-09-130-114-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/POCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-F1s  
US-08-232-463-14

Query Match 4.0%; Score 89; DB 1; Length 7218;

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Best Local Similarity 3.8%; Pred. No. 1.5e-13;
Matches 14; Conservative 242; Mismatches 117; Indels 0; Gaps 0;

QY 1274 AAGAAAACCATCGAGCTTCGCCGCGCAGGAAATGACCGTCGCTGTTGTCGATT 1333
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1414 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1355
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1334 TTCTGACCTATGTGAACCTCGACGATAAACCTGACGCCCAAGATTAACCAAGG 1393
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1354 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1295
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1394 CGGAAGATAAGGGAAGGATGAAGAGGATACAGGCGTTGGTAACGACGAAGACCGG 1453
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1294 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1235
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QY 1454 AAGATGAAGCCGACGAGGACGAGGAGGCGAAGCAAAATCGCGATGAAGAGGAG 1513
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Db 1234 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1514 GTGCGGAAGACGACCCGACGAAACGAGAGGCGGCGAAGACGAGCTGAAGACCTG 1573
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1174 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1115
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1574 AAGAACCCGAGAAGAAATCGCCGCGAGAGGCGGCGTGTGTTTCAGACGCATCCTGC 1633
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1114 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1055
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QY 1634 CCGCTCCGAGAC 1646
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1054 CTCGACCTGCAGC 1042

RESULT 2
US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-363 : polymorphic base A or G
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-363.misl, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-454-363.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 139..158
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
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; LOCATION: 634..652
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-454-363 potential probe
; NAME/KEY: misc feature
; LOCATION: 674..679,881..882,892..893
; OTHER INFORMATION: n=a, g, c or t
US-09-671-317-14

Query Match 3.4%; Score 75; DB 4; Length 929;
Best Local Similarity 59.7%; Pred. No. 2.8e-10;
Matches 138; Conservative 0; Mismatches 91; Indels 2; Gaps 1;

QY 1397 AAGATAAAGGGAAGATGAAGAGATACAGGCTTGGTAACGACGAAGACCGGAG 1456
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Db 872 AAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 813
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1457 ATGAAGCCGACGAGCGAAGAGGCGAAGACGAAATCGCGATGAAGGAGGAGTG 1516
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 812 AAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 753
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QY 1517 CGAAGACGAAAGCCGACGAAACGAGGCGGCGAAGACGAACTGAAGAACTGAG 1576
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Db 752 AAGAAGAAGAAGAAG- -GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 695
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QY 1577 AACCCGAAGAAGATCGCCGCGCAGAGGCGGCGTGTGTTTCAGACGCA 1627
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Db 694 AAGAAGAAGAAGAAGNANNNNNNAAGAAGAAGAAGATGCCGTGCTACTGAA 644

RESULT 3
US-09-671-317-439/c
; Sequence 439, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 439
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-242 : deletion AT
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-242.misl, potential
; NAME/KEY: primer_bind
; LOCATION: 260..279
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 755..773
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc feature
; LOCATION: 795..800
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[illegible]

RESULT 7  
US-08-781-891-208/c  
; Sequence 208, Application US/08781891  
; Patent No. 6090620  
; GENERAL INFORMATION:  
; APPLICANT: Fu, Ying-Hui  
; APPLICANT: Yu, Chang-En  
; APPLICANT: Oshima, Junko  
; APPLICANT: Mulligan, John T.  
; APPLICANT: Schellenberg, Gerald D.  
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO  
; TITLE OF INVENTION: WERNER'S SYNDROME  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
;

	Query Match	3.1%;	Score 69.8;	DB 3;	Length 16442;
	Best Local Similarity	60.9%;	Pred. No. 3.6e-08;		
	Matches 131;	Conservative 0;	Mismatches 82;	Indels 2;	Gaps 1;
QY	1391	AGGCGGAAGATAAAGGGAGGATGAAGAGGATACAGGGCTTGTTAACGCAG--AGAAGG	1448		
Db	16335	AGGAGGAGGAGGAGCAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	16276		
QY	1449	CACGGAAGATGAAGCCGCNAGAAGGCCAGCGAAGAGCGCAAAATCGGCGATGAAGG	1508		
Db	16275	AGCAGGAGGAGGAGGAGCAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG	16216		
QY	1509	AGGAGGTGCGGAAGACGAAGCCGACAGAAAACGAAGCGCGAAGAGACAGACTGAACA	1568		
Db	16215	AGGAGGAGGAGAGTGAAGGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGA	16156		
QY	1569	ACCTGAAGAACCCGAGAGAGAATCCCGCAGAAG	1603		
Db	16155	AGAAGGAG	16121		

RESULT 9  
US-09-177-325-2  
; Sequence 2. Application US/09177325B  
; Patent No. 6214983  
; GENERAL INFORMATION:  
; APPLICANT: Tureci, Ozlem

```

RESULT 8
US-09-618-166-208/c
; Sequence 208, Application US/09618166
; Patent No. 6583112
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; Yu, Chang-En
; Oshima, Junko
; Mulligan, John T.
; Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US/09/618,166
; FILING DATE: 17-Jul-2000
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.419C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4300
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-09-618-166-208

Query Match 3.1%; Score 69.8; DB 4; Length 16442;
Best Local Similarity 60.9%; Pred. No. 3.6e-08;
Matches 131; Conservative 0; Mismatches 82; Indels 2; Gaps 1;

QY 1391 AGCGGNAGTAAGCGGAGGATGAAGAGATACAGCGCTTGGTACGACGA--AGAAG 1448
Db 16335 AGGAGGAGGAGGAGGAGCAGCGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 16276
QY 1449 CACGGAAGATGAAGCCGCGAGAGCGACGAGCGGAGAGACGAATCGGCGATGAAG 1508
Db 16275 ACAGAGGAGGAGGAGCAGCGAGGAGCAGCGAGGAGGAGGAGGAGGAGGAGGAGG 16216
QY 1509 AGGAGGTGCGGAGACGAAGCCGCGCAGAAACGAACGAGCGCGGCGGAGAGACGAGCTGAAGA 1568
Db 16215 AGGAGGAGGAGGAGTAGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 16121
QY 1569 ACCTGAAGAACCCGAGAGAGATCGCCGCGAGAAG 1603
Db 16155 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 16121

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RESULT 9  
US-09-177-325-2  
; Sequence 2. Application US/09177325B  
; Patent No. 6214983  
; GENERAL INFORMATION:  
; APPLICANT: Tureci, Ozlem

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; APPLICANT: Sakin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins, And
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: LUD 5525
; CURRENT APPLICATION NUMBER: US/09/177,325B
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 2
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-177-325-2

Query Match
Best Local Similarity 3.1%; Score 68.2; DB 3; Length 1276;
Matches 124; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1386 ACCAAAGGCGGAAGATTAAGGGAAGGATGAAGAGGATACAGCGTTGGTTAAGCAAGAA 1445
Db 713 AGCAGCAGCAGAAAGTAATAGTAGTAAGACGAAGAGGAGGAAGAGAGGAGGAGGA 772

QY 1446 AGGCACCGAAGATGAAGCCGCGAAGGCGAGGCGGAAGACCAAAATCGGCGATGA 1505
Db 773 GGAGAAAGAGAGGAGGAGGAAGAGAGGAGGAAGAGAGGAGGAGGAGGAAGA 832

QY 1506 AGGAGGAGGTGCGGAAGACGAAAGCCGCGAGAAACGAAGCGCGGAGAAAGAAAGCAAGCTGA 1565
Db 833 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 892

QY 1566 AGAAGCTGAAGAACCCGGAAGAGATCGCGGCAGAA 1602
Db 893 GGAAGAGGAGGAACCAAAATTAAGCATTTCAAGAAAAA 929

RESULT 10
US-09-411-812A-2
; Sequence 2, Application US/09411812A
; Patent No. 6261778
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins, And
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: LUD 5525.1 CIP
; CURRENT APPLICATION NUMBER: US/09/411,812A
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 09/177,325
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-411-812A-2

Query Match
Best Local Similarity 3.1%; Score 68.2; DB 3; Length 1276;
Matches 124; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1386 ACCAAAGGCGGAAGATTAAGGGAAGGATGAAGAGGATACAGCGTTGGTTAAGCAAGAA 1445
Db 713 AGCAGCAGCAGAAAGTAATAGTAGTAAGACGAAGAGGAGGAAGAGAGGAGGAGGAGGA 772

QY 1446 AGGCACCGAAGATGAAGCCGCGAAGGCGGAAGACCAAAATCGGCGATGA 1505
Db 773 GGAGAAAGAGAGGAGGAGGAAGAGAGGAGGAAGAGAGGAGGAGGAGGAAGA 832

QY 1506 AGGAGGAGGTGCGGAAGACGAAAGCCGCGAGAAACGAAGCGCGGAGAAAGAAAGCAAGCTGA 1565
Db 833 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 892
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QY 1566 AGAAGCTGAAGAACCCGGAAGAGATCGCGGCAGAA 1602
Db 893 GGAAGAGGAGGAACCAAAATTAAGCATTTCAAGAAAAA 929

RESULT 11
US-09-590-113-2
; Sequence 2, Application US/09590113
; Patent No. 6306389
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sakin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode SCP Proteins, And
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: LUD 5525
; CURRENT APPLICATION NUMBER: US/09/590,113
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/177,325
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 2
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-590-113-2

Query Match
Best Local Similarity 3.1%; Score 68.2; DB 4; Length 1276;
Matches 124; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1386 ACCAAAGGCGGAAGATTAAGGGAAGGATGAAGAGGATACAGCGTTGGTTAAGCAAGAA 1445
Db 713 AGCAGCAGCAGAAAGTAATAGTAGTAAGACGAAGAGGAGGAAGAGAGGAGGAGGA 772

QY 1446 AGGCACCGAAGATGAAGCCGCGAAGGCGAGGCGGAAGACCAAAATCGGCGATGA 1505
Db 773 GGAGAAAGAGAGGAGGAGGAAGAGAGGAGGAAGAGAGGAGGAGGAGGAAGA 832

QY 1506 AGGAGGAGGTGCGGAAGACGAAAGCCGCGAGAAACGAAGCGCGGAGAAAGAAAGCAAGCTGA 1565
Db 833 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 892

QY 1566 AGAAGCTGAAGAACCCGGAAGAGATCGCGGCAGAA 1602
Db 893 GGAAGAGGAGGAACCAAAATTAAGCATTTCAAGAAAAA 929

RESULT 12
US-09-197-649-7
; Sequence 7, Application US/09197649
; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk, Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/C1-CON
; CURRENT APPLICATION NUMBER: US/09/197,649
; CURRENT FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: 07/829,461
; EARLIER FILING DATE: 1992-01-31
; EARLIER APPLICATION NUMBER: 07/739,055
; EARLIER FILING DATE: 1991-08-01
; EARLIER APPLICATION NUMBER: 07/561,968
; EARLIER FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match      3.0%; Score 66.8; DB 3; Length 390;
Best Local Similarity 55.0%; Pred. No. 2.8e-08;
Matches 131; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1391 AGCGCGAAGATAAAGGGAAGGATGAAGAGATACAGGCGTTGTGTAAACGACGAAGAGGCA 1450
Db 136 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 195
QY 1451 CGGAGATGAAGCGGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGGAG 1510
Db 196 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 255
QY 1511 GAGGTGCGGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1570
Db 256 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 315
QY 1571 CTGAGAAACCCGAGAGAAATCCCGGCGAGAGGCGGCGGTGTTGTTTCAGACGGCAT 1628
Db 316 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 373

RESULT 13
US-08-574-959A-8
; Sequence 8, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
US-08-574-959A-8

Query Match      2.9%; Score 65; DB 2; Length 3211;
Best Local Similarity 53.8%; Pred. No. 2.8e-07;
Matches 134; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 1376 CAGCAAGTAAACCAAGCGGGAAGATTAAGGAAGGATGAAGAGGATACAGCGTTGGTA 1435
Db 2372 CAGTTATTATATCAACAGCAGTCAGTATGAAGAGGAGGAGGAAGGAAGGAAGAAG 2431
QY 1436 ACGACGAGAAGCGACGGAAGATGAAGCGCGAGAGGCGAGCGAGGAGGAGGAGGAGG 1495
Db 2432 AAGAAGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2491
QY 1496 TCGGCGATGAAGAGGAGGTGCGGAAGACGAAACCGCGCAAAACGAAAGCGCGGAGAG 1555
Db 2492 TTGAGGAAGAGGAGGAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2551
QY 1556 ACGAGCTGAAGAACCTGAGAACCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1615
Db 2552 AGTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2611
QY 1616 GTTCAGACG 1624
Db 2612 ATGAGGAGG 2620

RESULT 14
US-09-357-014-8
; Sequence 8, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/357,014
; FILING DATE: 19-Jul-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/574,959
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-357-014-8
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Query Match	2.9%;	Score 65;	DB 3;	Length 3211;
Best Local Similarity	53.8%;	Pred. No. 2.8e-07;		
Matches 134;	Conservative	0;	Mismatches 115;	Indels 0;
Gaps	0;			
QY	1376	CAGCAAGTAAACCAAAAGGCGGAAGATAAAGGGGAAGGATGAAGAGGATACAGGCGTTGGTA	1435	
Db	2372	CAGTTATTATATCAACAGCAGTGATGAAGAGGAGGGAAGAGGAGGAAGAGGAAGAAG	2431	
QY	1436	ACGACGAAGNAGGCA CGGAGATGAGCCGACAGAGGCAGGAGGCGGAGACGAAA	1495	
Db	2432	AAAGAAGAAGAAGAAAGAGAGGAAGAAGAAAGAGGAAAGAGGAGGAAGACT	2491	
QY	1496	TCGCGCATGAAGGAGGAGGTGCGGAAGACGAAGCCGACAGAAAACGAAGCGGCGCAAGAAG	1555	
Db	2492	TTGAGGAAGAGGAAGAGGATGAAGAGGAATATTTTGAAGAGGAAGAAGACGAGGAAGAAG	2551	
QY	1556	ACGAAGCTGAGAACCTGAGAACCCGAAGAAGATCGCCGCGACAGAGGCGGCGGTG	1615	
Db	2552	AGTTTGAGGAGAGAAATTTGAGGAAGAAGGTTGAGTGTAGAGGAAGAAGAAGAAGAGG	2611	
QY	1616	GTTCAGACG	1624	
Db	2612	ATGAGGAGG	2620	

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RESULT 15
US-08-574-959A-6
; Sequence 6, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Young, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p02 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/POCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3901 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3847
US-08-574-959A-6

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Query Match      2.9%; Score 65; DB 2; Length 3901;
Best Local Similarity 53.8%; Pred. No. 3.2e-07;
Matches 134; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
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Qy	1376	CACCAAGTAAACCAAAGCGGGAATAAAGGNAGGATGAAGAGGATACAGGGCTTGGA	1435
Dd	3062	CAGTTTATTATATCAAACAGCAGTGTGAAGAGAGGAGGAAGAAGAGGAAGAAG	3121
Qy	1436	ACCACGAAGAAGGCACGGAAGATGAAGCCGACGACCGAAGGAGGCCAAGACGAAA	1495
Dd	3122	AAGAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGNAGACT	3181
Qy	1496	TCCGCGATGAAGGAGGAGGTTCGGAGACGAGCCCGAGAAACGAAGGCCGCGAAGAAG	1555
Dd	3182	TTGAGGAAGAGGGAAGAGGATGAAGAGGAAATATTTTGAAGAGGAAGAAGAGGAGGAAGAAG	3241
Qy	1556	ACGAAGCTGAAGAACCTGAAGAACCCCGAAGAAATCCCGGCAGAGGCGCGCGTGTG	1615
Dd	3242	AGTTTTGAGNAGAAATTTGAGCAAGAGAGGTTCAGTTAGNAGGAAGAAGAGAGGAGG	3301
Qy	1616	GTTCCAGACG	1624
Dd	3302	ATGAGGAGG	3310

Search completed: August 25, 2004, 05:32:05  
Job time : 163.734 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 11:49:00 ; Search time 5079.42 Seconds  
(without alignments)  
13086.780 Million cell updates/sec

Title: US-10-735-098-5

Perfect score: 2226

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Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
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11: gb\_hic:\*  
12: gb\_est3:\*  
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14: gb\_est5:\*  
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23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	92.4	4.2	434	14	CA745444
3	92.4	4.2	980	13	BU944408
C 4	91.8	4.1	263	13	BU005139

5	91.8	4.1	665	13	BU432980
C 6	91.8	4.1	1096	14	CK206118
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8	91.4	4.1	341	29	CE510654
9	91	4.1	264	13	BQ241566
C 10	90.2	4.1	691	28	BH040136
11	89.8	4.0	358	28	AZ582992
C 12	89.8	4.0	617	28	AZ296172
C 13	89.4	4.0	232	29	CG321416
C 14	89.4	4.0	605	28	BZ222147
C 15	89.2	4.0	311	14	CA699402
C 16	89.2	4.0	617	14	CA743799
C 17	89	4.0	697	28	AZ374916
C 18	88.4	4.0	575	10	BF707975
C 19	88.4	4.0	739	28	BZ220379
C 20	88.4	4.0	879	28	AZ550718
C 21	88.4	4.0	942	28	BH148582
C 22	88.4	4.0	3743	11	AK048184
C 23	88.2	4.0	265	14	CA607797
24	88.2	4.0	540	28	AZ813205
25	88.2	4.0	634	28	AZ008814
26	88	4.0	332	14	CA566759
27	87.8	3.9	278	13	BQ460618
28	87.6	3.9	477	14	CD311846
29	87.6	3.9	531	14	CD915362
30	87.6	3.9	571	28	AZ952930
31	87.4	3.9	633	28	AZ855793
32	87	3.9	447	9	AA110445
33	87	3.9	466	28	AZ296286
34	86.8	3.9	799	28	BZ201507
C 35	86.8	3.9	880	28	AZ529191
36	86.6	3.9	223	13	CA022136
C 37	86.6	3.9	289	14	CA716220
C 38	86.6	3.9	906	28	BH153606
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## ALIGNMENTS

RESULT 1  
CE760553

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

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genomic survey sequence.  
CE760553  
CE760553.1 GI:37101172  
GSS  
Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 395)  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
22875432  
14512627  
Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org

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CK206118 FGAS01769  
CC143364 NDL.32A.3  
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BQ241566 TaE05003E  
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AZ952930 2M0217N19  
AZ855793 2M0160B03  
AA110445 ml61d06.r  
AZ296286 RPCI-23-1  
BZ201507 CH230-445  
AZ529191 ENTPV68TR  
CA022136 HZ42E07r  
CA716220 wdk3c.pk0  
BH153606 ENTIS83TF  
BQ925195 AGENCOURT  
BQ459561 HA08M06r  
BU976670 HA10B15r  
BQ462203 HD02A20r  
BZ104011 CH230-227  
AZ527885 ENTPA79TR  
BH146886 ENTPK48TF

(susceptible) wheat leaves infected with *Septoria tritici* strain A, 48 hours after infection, subtracted w/ comparable uninfected leaves"

```

Class: shotgun.
      Location/Qualifiers
1. 395
   /organism="Canis familiaris"
   /mol_type="genomic DNA"
   /strain="Standard Poodle"
   /db_xref="taxon:9615"
   /clone_lib="Dog Library"
   /note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

```

[illegible][illegible]

ACCESSION	BU944408		
VERSION	BU944408.1	GI:24133227	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa;		
	Chordata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria;		
	Primates; Catarrhini; Hominoidea; Homo.		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 980)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabos-r@mail.nih.gov">cgabos-r@mail.nih.gov</a> Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>			
	Plate: LLCM3050	row: k	column: 11	
	High quality sequence start: 11			
	High quality sequence stop: 690			

```

FEATURES
source
Location/Qualifiers
1..980
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6728676"
/tissue_type="adenocarcinoma, cell_line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/notes="Organ: breast; Vector: pOTF7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Suratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
```

## ORIGIN

RESULT 2	EST 26-NOV-2002
CA745444/c	
LOCUS	434 bp
CA745444	linear
wri2s.pk001.i6	Triticum aestivum cdna clone wri2s.pk001.i6 5'
DEFINITION	end, mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CA745444	CA745444.1	EST.	Triticum aestivum (bread wheat)	
CA745444			Triticum aestivum	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticeae; Triticum.	

REFERENCE  
AUTHORS  
TITLE  
COMMENT

1 (bases 1 to 434)  
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
Miao, G., Caraher, N. and Hanafey, M.K.  
DuPont Wheat cDNA Sequence  
Unpublished (2002)  
Contact: Scott V. Tingey  
Crop Genetics  
E. I. DuPont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: T7.

```

FEATURES
source
Location/Qualifiers
1..434
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wri2s pk001.i6"
/tissue_type="leaf"
/lab_host="DH10B"
/clone_lib="wri2s"
/note="Vector: pGEM-T Easy; Site 1: SmaI; Riband

```

```

/clone_11d-w1128
/note="Vector: PGEM-T Easy; Site 1: SmaI; Riband

```



Query Match 4.2%; Score 92.4; DB 13; Length 980;  
 Best Local Similarity 55.9%; Pred. No. 3.3e-07;  
 Matches 147; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1385 AACCAAGCGGAAGATAAGGAAGGATGACAGAGATACAGCGTGTGGTAACGACGAAG 1444  
 |||  
 Db 483 AAGAAGAAG 542  
 |||

QY 1445 AAGGACAGGAAGATGAAGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1504  
 |||  
 Db 543 AAGAAGAAGGAG 602  
 |||

QY 1505 AAGGAGAGGTCGCGAAGAGAGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1564  
 |||  
 Db 603 AAGGAG 662  
 |||

QY 1565 AAGAACCTGGAAGAACCCGAGAGAGAGATCGCCGAGAGAGAGAGAGAGAGAGAGAGAG 1624  
 |||  
 Db 663 AAGAAGAAG 722  
 |||

QY 1625 GCATCTGCTGCCCTCGGAGAGCT 1647  
 |||  
 Db 723 GCCGCTCGGCCCTCGAGAGCT 745  
 |||

RESULT 4  
 BU005139/c  
 LOCUS QG7D20.YG.abi OG EFGHJ lettuce serriola Lactuca sativa cDNA clone  
 DEFINITION QG7D20, mRNA sequence.  
 ACCESSION BU005139  
 VERSION BU005139.1 GI:22439534  
 KEYWORDS EST.  
 SOURCE Lactuca sativa  
 ORGANISM Lactuca sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
 Cichorieae; Lactuca.  
 1 (bases 1 to 263)  
 Kozik, A., Michelmore, R.W., Knapp, S., Mattvienko, M., Rieseberg, L.,  
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
 Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
 Lai, Z., Church, S., Jackson, L. and Bradford, K.  
 Lettuce and Sunflower ESTs from the Compositae Genome Project  
 http://comgenomics.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmundson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]  
 singleton, see http://cgpdb.ucdavis.edu/ for details.  
 Plate: QG7 row: D column: 20.

## FEATURES

Location/Qualifiers  
 1..263  
 /organism="Lactuca sativa"  
 /mol\_type="mRNA"  
 /cultivar="L.serriola"  
 /db\_xref="taxon:4236"  
 /clone="QG7D20"  
 /lab\_host="E.coli"  
 /clone\_lib="QG EFGHJ lettuce serriola"

/note="Vector: pBRCDNASFIAB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library

## ORIGIN

Query Match 4.1%; Score 91.8; DB 13; Length 263;  
 Best Local Similarity 60.7%; Pred. No. 4e-07;  
 Matches 150; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1362 AAAAACTGACCCCGAGCAAGTAAACCAAGCGGAAGATAAAGGAGGATGAAGAGGA 1421  
 |||  
 Db 262 ACAGACAGAAACAG 203  
 |||

QY 1422 TACAGCGGTGTGTAACGACGAAGAGGCGACGGAAGATGAAGCCGAGAGAGCGCGAAGG 1481  
 |||  
 Db 202 AGAAGAAG 143  
 |||

QY 1482 AGGCCGAGAGCAAGTAATCGCGATGAGGAGGAGGTGGGAGAGACGAGCCGCGAAGACGA 1541  
 |||  
 Db 142 AGAAGAAG 83  
 |||

QY 1542 AGCGCGCGAAG 1601  
 |||  
 Db 82 AGACGAG 23  
 |||

QY 1602 AGCGCGC 1608  
 |||  
 Db 22 AGAAGAC 16  
 |||

## RESULT 5

BU432980  
 LOCUS 603221001F1 CSEQRBNI0 Gallus gallus cDNA clone ChEST215a2 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BU432980  
 VERSION BU432980.1 GI:25922291  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 665)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 2233534  
 12445392

## COMMENT

Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

## source

Location/Qualifiers  
 1..665  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="ChEST215a2"  
 /sex="Male and female"  
 /tissue\_type="Chondrocytes isolated from growth plate cartilage"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQRBNI0"  
 /note="Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated

construction can be obtained at [http://cgpdb.ucdavis.edu/TAG\\_SEQ=Not found](http://cgpdb.ucdavis.edu/TAG_SEQ=Not found)

using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 4.1%; Score 91.8; DB 13; Length 665;  
 Best Local Similarity 60.7%; Pred. No. 4.2e-07;  
 Matches 150; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1378 GCAAGTAAACCAAGCGGGAAGATAAAGGGAAGGATGAAGAGGATACAGGCGTTGGTAAC 1437  
 DB 21 GAAGATGAGATGAGAGAGAGATGAAGAGAGATGAAGATGAAGATGAAGAT 80

QY 1438 GACGAAGAGGACCGGAAGATGAAGCCGAGAGGCGGAGAGGCGGAAGCAATC 1497  
 DB 81 GAAGAAGAAGATGAAGAAGAGATGAAGAAGAGATGAAGAAGAGATGAAGAAGAT 140

QY 1498 GCGGATGAAGGAGGTCGGAAGACGAGCGGAGAGAAAGGCGGCGGAAGAGAC 1557  
 DB 141 GAAGAAGAAGAAGAAGAAGAAGATGAAGAAGATGAGATGACCAAGAGAT 200

QY 1558 GAACTGGAAGACCTGAAGAACCGGAAGAGATCGCGGAGAGGCGGCGTGTGTG 1617  
 DB 201 GAAGATGAGATGAAGAAGAGATGAAGAAGATGAAGAAGAGACCAAGATGACGAA 260

QY 1618 TCAGACG 1624  
 DB 261 GAAGATG 267

## RESULT 6

CK206118/1096 bp mRNA linear EST 08-DEC-2003  
 FGAS017695 Triticum aestivum FGAS: Library 5 GATE 7 Triticum  
 aestivum cDNA, mRNA sequence.

CK206118  
 CK206118.1 GI:39568508

EST.  
 Triticum aestivum (bread wheat)

ORGANISM  
 Triticum aestivum

DEFINITION  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.

LOCUS  
 1 (bases 1 to 1096)

REFERENCE  
 Allard, F., Crosby, W.D., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,  
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
 Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,  
 Penniket, C., Roach, J.L. and Sarhan, F.  
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops  
 Unpublished (2003)

TITLE  
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops

JOURNAL  
 Unpublished (2003)

COMMENT  
 Contact: Mm I. Crosby

Bioinformatics  
 University of Saskatchewan, Department of Computer Science  
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
 Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas\_estcs@usask.ca

This sequence is the direct result of the Base calling software  
 Phred (default parameters). It is the raw base calls. To aid in the  
 identification of the high quality insert the software Lucy  
 (default parameters) has been run on this sequence. Lucy identified  
 the region [29,696].

Plate: L5B006 row: F column: 12.

Location/Qualifiers

## FEATURES

## source

1. 1096  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4565"  
 /clone\_lib="Triticum aestivum FGAS: Library 5 GATE 7"  
 /note="Vector: pCMV.SPORT6; Crown and developmental stages  
 of spike formation in wheat cultivar Norstar. 4 mRNA  
 populations were combined before constructing the library.  
 The first mRNA population is from lcm crown sections after  
 30 days of cold acclimation. The second is from lcm crown  
 sections after 11 days of deacclimation (before  
 deacclimation plants were fully vernalized for 49 days).  
 The third is from different developmental stages of spike  
 formation (5 to 50mm) that still have not emerged from the  
 leaf (dissection required). The last is from different  
 developmental stages of spike and seed formation after  
 having emerged from the leaf (visible). First strand  
 synthesis in this library was done in the presence of  
 methylated dCTP thereby protecting from internal cleavage  
 with NotI."

## ORIGIN

Query Match 4.1%; Score 91.8; DB 14; Length 1096;  
 Best Local Similarity 59.3%; Pred. No. 4.4e-07;  
 Matches 156; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1362 AAAAATGACCCCGCAGCAAGTAAACCAAGCGGAGATGAAGGAGGATGAAGAGCA 1421  
 DB 297 ACAAGAAGCACCAGCAGCAGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 238

QY 1422 TACAGCGCTGTGTAACGACGAGAGGCGCAAGATGAAGCCGAGAGGCGGAGG 1481  
 DB 237 AGAAGAAG 178

QY 1482 AGCGCAAGACGAAATCGCGATGAAGAGAGAGGTCGCGGAGAGCGAGAGCGCGAGAAACGA 1541  
 DB 177 AGAAGAAG 118

QY 1542 AGCGCGCGAG 1601  
 DB 117 AGAAGAAG 58

QY 1602 AGCGCGCGGT 1624  
 DB 57 AGGAG 35

## RESULT 7

CC143364

LOCUS

DEFINITION

NDL.32A13.T7 Notre Dame Liverpool Aedes aegypti genomic clone

CC143364

ACCESSION

VERSION

CC143364.1 GI:30012419

KEYWORDS

SOURCE

Aedes aegypti (yellow fever mosquito)

ORGANISM

Aedes aegypti

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Megaloptera; Diptera; Nematocera; Culicoidae; Aedes;

Stegomyia.

REFERENCE

1 (bases 1 to 960)

AUTHORS

Loftus, B., Shetty, J., Knudson, D. and Severson, D.

TITLE

BAC end sequencing of Aedes aegypti

JOURNAL

Unpublished (2003)

COMMENT

Other\_GSSs: NDL.32A13.SP6

Contact: Brendan Loftus

Department of Eukaryotic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: enta@tigr.org

Library was provided by David Severson

```
Seq primer: T7
Class: BAC ends.
FEATURES
    source
        Location/Qualifiers
            1..960
                /organism="Aedes aegypti"
                /mol_type="genomic DNA"
                /strain="liverpool"
                /db_xref="taxon:7159"
                /clone="NDL32Al3"
                /clone_lib="Notre Dame Liverpool"
                /note="Vector: pECBAC1; Site 1: Hind III; The library was
                prepared from whole body tissue of newly hatched L1 larvae
                by David Severson at the University of Notre Dame and
                Hongbin Zhang"
ORIGIN
Query Match          4.1%; Score 91.6; DB 28; Length 960;
Best Local Similarity 59.0%; Pred. No. 4.7e-07;
Matches 157; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
QY 1387 CCAAGGCGGAGATTAAGCGGAGGATGAAGAGGATACAGCGTGTGTTAACGACGAAGAA 1446
Db 425 CAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 484
QY 1447 GGCACGGAATGAAGCCCGCAGAAAGCGACGAGGAGCGAAGACGAAATCGCGATGAA 1506
Db 485 GAAGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 544
QY 1507 GGAGAGGTGCGGAGACGAGACCGCGCAGAAAACGAAAGCGCGGAGAGACCAAGCTGAA 1566
Db 545 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGNA 604
QY 1567 GNACTTGAGACCCGAGAGAAATCCCGCGCAGAGAGCGCGGTGTTTCAGACGGC 1626
Db 605 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTGTAGTGG 664
QY 1627 ATCTGCGCGCTCCGAGCTCTTAA 1652
Db 665 TTCCCAAGCGCCCTGAAGGTATTAA 690
RESULT 8
LOCUS CE510654 341 bp DNA linear GSS 28-SEP-2003
DEFINITION tigr-gss-dog-17000327383461 Dog Library Canis familiaris genomic,
Genomic survey sequence.
ACCESSION CE510654
VERSION CE510654.1 GI:36827435
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Kirkness,B.F., Bafna,V., Halpern,A.L., Levv,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
    source
        Location/Qualifiers
            1..341
                /organism="Canis familiaris"
                /mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
ORIGIN
Query Match          4.1%; Score 91.4; DB 29; Length 341;
Best Local Similarity 62.4%; Pred. No. 4.8e-07;
Matches 143; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1385 AACCAAGCGGAGATTAAGGAGGAGGATGAAGAGATACAGCGTGTGTTAACGACGAAG 1444
Db 1 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 60
QY 1445 AAGGACGAGAGATGAAGCCCGCAGAAAGCGCAGGAGGCGGAGAGCAATCGCGGATG 1504
Db 61 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG 120
QY 1505 AAGGAGGAGGTGCGGAGACGAGCGCGCAGAAAACGAAAGCGCGGAGAGACCAAGCTG 1564
Db 121 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAGG 180
QY 1565 AAGAACCTTGAAGAACCCGAGAGAAATCGCGCGCAGAGAGCGCGGTGG 1613
Db 181 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAGGAGG 229
RESULT 9
LOCUS BQ241566 264 bp mRNA linear EST 03-MAY-2002
DEFINITION Ta050003E07R Tae05 Triticum aestivum cDNA clone Tae05003E07R, mRNA
sequence.
ACCESSION BQ241566
VERSION BQ241566.1 GI:20437442
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 264)
Cloutier,S.
Wheat functional genomics - Glenlea developing seeds cDNA libraries
Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 003 row: E column: 07
Seq primer: M13 Reverse.
FEATURES
    source
        Location/Qualifiers
            1..264
                /organism="Triticum aestivum"
                /mol_type="mRNA"
                /cultivar="Glenlea"
                /db_xref="taxon:4565"
                /clone="Tae05003E07R"
                /tissue_type="developing seeds"
                /dev_stage="5 days after anthesis"
                /lab_host="E. coli DH10B"
                /clone_lib="Tae05"
                /note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
                NotI; Site 2: MluI; mRNA obtained from wheat seeds of
                cultivar Glenlea 5 days post-anthesis"
ORIGIN
Query Match          4.1%; Score 91; DB 13; Length 264;
```

Best Local Similarity 63.5%; Pred. No. 5.7e-07;  
Matches 139; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1385 AACCAAGCGGGAAGATAAGGAGGATGAAGAGGATACAGCGCTGGTAAACGAGAG 1444  
DB 22 AAGAGAGAGTGAAG 81  
QY 1445 AAGGACAGGAGATGAAGCGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1504  
DB 82 AAG 141  
QY 1505 AAGGAGAGAGTGGAG 1564  
DB 142 AAG 201  
QY 1565 AAG 1603  
DB 202 AAG 240

RESULT 10  
BH040136/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BH040136  
RPCI-24-255A23.TV RPCI-24 Mus musculus genomic clone  
RPCI-24-255A23, genomic survey sequence.  
BH040136  
GSS.  
BH040136.1 GI:14818806  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 691)  
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,  
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,  
Russell, D., de Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from Library RPCI-24  
Unpublished (1999)  
Other\_GSSs: RPCI-24-255A23.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-24. For BAC  
library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org). Clones may be purchased from BACPAC  
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end  
page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
Plate: 255 row: A column: 23  
Seq primer: T7  
Class: BAC ends.

FEATURES  
source  
1. .691  
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DNA."

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Best Local Similarity 58.9%; Pred. No. 8.5e-07;

Matches 155; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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VERSION  
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ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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clone UUGCIM0376K12 R, genomic survey sequence.  
AZ582992  
GI:11702428  
GSS.  
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niedermauern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Class: plasmid ends  
High quality sequence stop: 358.

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(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4











GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:53:30 ; Search time 8482.05 Seconds  
(without alignments)  
11558.757 Million cell updates/sec

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Perfect score: 2262  
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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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22: em.ov.\*

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and is derived by analysis of the total score distribution.

# SUMMARIES

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3	2262	100.0	2262	6	A98974 Sequence 7
4	1558	68.9	9955	1	BD074758 Neisseria
5	1558	68.9	349980	6	AE002504 Neisseria
6	1465.2	64.8	2277	1	AX044033 Sequence
7	1465.2	64.8	2277	1	AF022781 Neisseria
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9	1465.2	64.8	2277	6	BD074755 Neisseria
10	1463.6	64.7	5691	1	AF049349 Neisseria
11	1442.6	63.8	326301	1	AF031432 Neisseria
12	1442.2	63.8	2226	1	AF123380
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38	105	4.6	213739	2	AC113937
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# ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

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Neisseria meningitidis strain m990  
precursor (lbpB) gene, complete cds.  
AF123381  
AF123381.1 GI:4884688

Neisseria meningitidis  
Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
1 (bases 1 to 2262)  
Pettersson, A., van der Biezen, J., Joosten, V., Hendriksen, J. and  
Tommassen, J.

Pred. No. is the number of results predicted by chance to have a

TITLE Sequence variability of the meningococcal lactoferrin-binding protein lbpB  
JOURNAL Gene 231 (1-2), 105-110 (1999)  
MEDLINE 99250255  
PUBMED 10231574  
REFERENCE 2 (bases 1 to 2262)  
AUTHORS Pattersoh, A., van der Biesen, J., Joosten, V., Hendriksen, J., and Tomassen, J.

TITLE Direct Submission  
JOURNAL Submitted (06-JAN-1999) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands  
FEATURES Location/Qualifiers

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ORIGIN

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VERSION A98974.1 GI:6781934  
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Neisseriaceae; Neisseria.  
1 (bases 1 to 2262)  
Pettersson-Fernholm, A.M. and Tommassen, J.P.  
TITLE NEISSERIA LACTOFERRIN BINDING PROTEIN  
AUTHORS Patent: WO/9909176-A 7 25-FEB-1999;  
JOURNAL UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNKA MAX (NL)  
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ORIGIN

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Db	961	TTTTTCCATGCCGATGCCGATCAGCGCTTGAGGCGGTTTTTTCGGCGATTAACGGAGAA	1020
QY	1021	GAGCTTGGCGGACGGTTTATCAGCAACGACACAGCGTATTCGGCGTATTCGACGCAAA	1080
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QY	1741	ACCGGCACTTGGGAGCGGATCGGCAACCCCATTTCAATGGGACAAATCAGGCGGATGAA	1800
Db	1741	ACCGGCACTTGGGAGCGGATCGGCAACCCCATTTCAATGGGACAAATCAGGCGGATGAA	1800

RESULT 3

BD074758

LOCUS

Neisseria lactoferrin-binding protein.

DEFINITION

BD074758.1 GI:22620361

ACCESSION

JP 2001514894-A/4.

VERSION

unidentified

KEYWORDS

unclassified

SOURCE

unclassified

ORGANISM

1 (pages 1 to 2262)

REFERENCE

Felpholm, A.M.P. and Thomsen, J.P.M.

AUTHORS

Neisseria lactoferrin-binding protein

TITLE

Patent: JP 2001514894-A 4 18-SEP-2001;

JOURNAL

UNIVERSITY OF UTRECHT, TECHNOLOGY FOUNDATION

COMMENT

OS Unidentified

PN JP 2001514894-A/4

RD 18-SEP-2001

RF 10-AUG-1998 JP 2000509840

PP 15-AUG-1997 GB 9717423.9, 05-FEB-1998 GB 9802544.8 PI

PR ANICA MARGARETA PETERSON FELPHOLM, JOHANES PETRUS MARIA PI

THOMSEN

PC C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22,

PC C07K16/12,

PC C12N15/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC

C12N15/00

CC Strandedness: Double;

CC Topology: Linear;

CC Neisseria lactoferrin-binding protein

CC Location/Qualifiers

FT key

FT 1..2262

FT /organism='Unidentified'

FEATURES

source

1..2262

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BD074758

2262 bp

DNA

linear

PAT 27-AUG-2002



ORIGIN

Query Match									
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Matches 2262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	61	GGCGGCAATTTCCGGCGTACAGCCCTGTTGTCGAATCAACGCGGACCGGCCAACTCTGTCA	120						
QY	121	GATTCCAAATCTTTCCAAATCTCTGGGATAAGCCTGCTCCAGCTCTCTGCCAGACCTTCGGTA	180						
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DB	541	GGTTTTGTATATTTCGGAGAAAGTCTTCCCAATCTTTACCGAGTCGGGAAACGGTG	600						
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QY	661	GTTGGCATGTACAATTTGGGTTATATACATTTTATGTTAAGCATGTTGGTGCACTTCT	720						
DB	661	GTTGGCATGTACAATTTGGGTTATATACATTTTATGTTAAGCATGTTGGTGCACTTCT	720						
QY	721	TATGGGCTAAGGATGTCGACGAAGGAAAGCATCTGCCAATATACGGTTGATTTT	780						
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QY	781	GATAACAAAAACCATGAATGGCAAGTCGATTAATAATCAGTATGTCGGAATAAAAAAGAT	840						
DB	781	GATAACAAAAACCATGAATGGCAAGTCGATTAATAATCAGTATGTCGGAATAAAAAAGAT	840						
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LOCUS	Neisseria meningitidis serogroup B strain MC58 section 146 of 206 of the complete genome.				
ACCESSION	AE002504	AE002098			
VERSION	AE002504.1	GI:7226785			
KEYWORDS					
SOURCE	Neisseria meningitidis MC58				
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.				
REFERENCE	1 (bases 1 to 9955)				
AUTHORS	Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F., Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D., Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E., Citti, H., Vanathevan, J., Gill, J., Scariato, V., Maignani, V., Pappaoli, R., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappuoli, R., and Venter, J.C.				
TITLE	Complete genome sequence of Neisseria meningitidis serogroup B strain MC58				
JOURNAL	Science	287 (5459)	1809-1815	(2000)	
MEDLINE	20175755				
PUBMED	10710307				
REFERENCE	2 (bases 1 to 9955)				
AUTHORS	Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F., Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D., Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E., Citti, H., Vanathevan, J., Gill, J., Scariato, V., Maignani, V., Pappaoli, R., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappuoli, R., and Venter, J.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA				
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				Db	5484	AAACTTTAAAAGAAATCAACGACGSCATCTTAATGCACCAATCTACACGTTCGGATTTA	5425
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## ORIGIN

Query Match	68.9%	Score 1558;	DB 1;	Length 9955;
Best Local Similarity	83.6%;	Pred. No. 0;		
Matches 1906;	Conservative	0;	Mismatches 290;	Indels 84; Gaps 9;
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ORGANISM			

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.			
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Petersson, A., Prinz, T., Umar, A., van der Biezen, J. and  
Tommaassen, J.  
Molecular characterization of LbpB, the second lactoferrin-binding  
protein of Neisseria meningitidis  
Mol. Microbiol. 27 (3), 599-610 (1998)  
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Petersson, A., Prinz, T., Umar, A., van der Biezen, J. and  
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Direct Submission  
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Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands  
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Neisseriaceae; Neisseria.  
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Pettersson-Fernholm A.M. and Tommassen, J.P.  
NEISSERIA LACTOFERRIN BINDING PROTEIN  
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UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIE MAR (NL)  
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Matches 1835; Conservative 0; Mismatches 343; Indels 84; Gaps 8;  
QY 1 ATGTGTAAACCGCAATATGCGGCATTTGCTGTTGCCCTTACTTTTAGCATCTTGTATC 60  
Db 100 ATGTGTAAACCGCAATATGCGGCATTTGCTGTTGCCCTTACTTTTAGCATCTTGTATC 159  
QY 61 GCGGCAATTTCCGCGTACAGCCTGTTGTCGAATCAACGCGCACCGCGCAACTCTCTCA 120  
Db 160 GCGGCAATTTCCGCGTACAGCCTGTTGTCGAATCAACGCGCACCGCGCAACTCTCTCA 207  
QY 121 GATTCCAATCTTCCAAATCTGCGGATTAAGCCTGCTCCAGCTCTCCGAGCCTTCGGTA 180  
Db 208 TACCCCGTCACTTTCAAGTCTAAGGACGTTCCCACTCCGCCCTTCCCAACCTTCTATA 267  
QY 181 GAAATCACCGCGTCAAGCGCGCCGCGTGGTGGGCAATGCGGCTGCCAAGCGCGAAT 240  
Db 268 GAAATCACCGCGTCAAGCGCGCCGCGTGGTGGGCAATGCGGCTGCCAAGCGCGAAT 327  
QY 241 ATGCGCAATTTTGTATAAATGTTAATGAAATTTCCCAATAGTAAGCAGCAGAGGATAT 300  
Db 328 ACTGCTTTTTCATCGTGAAGTGGCAGCGAAATTTCCAAATAGCAACAGCAGAGGAAAG 387  
QY 301 CTGCGCCTCAAGAGAGAGGATATCTGTTTGTAGACGGTACGCGCAAGAAACAGGCTGAC 360  
Db 388 CTGCTGTTTCAAGAGGATGATGTTCTGTTTATACGGTTCAAAAGGAATTAACCTCAA 447  
QY 361 AAATCTTAAAGGAAATCAACGAGCGGATCTTAATGCAATCTAATGCAACCAATCTA 420  
Db 448 CAATCTTAAAGGAAATCTAATAACGATTCGATTCGATGTAGAAATTAGGACATCAGAAA 507  
QY 421 AAAGATGATGCGTATCAATATAAATATGTCGCGCGCGGATATGTTTATCTAGATATGSA 480  
Db 508 GAAATAAATAAATATGATTAATAATTTGTAGTGCAGGTTATGTATA---TGTAAGGGA 564  
QY 481 ACAGATGAATTCGAACAGAACTCAGCGCGTGAAGCGGTTACCCACCGCTTAGTTATGAC 540  
Db 565 AAAGATGAATTAAGTGAAGTTCAGATTAACGAGATTTTCCAAACGCTTAGTTATGAC 624  
QY 541 GGTTTGTATATATTCGCGAGACGTCCTTCCCAATCTTTACGAGTGCAGGAAACGGTG 600  
Db 625 GGTTTGTATATATTCGCGAGACGTCCTTCCCAATCTTTACGAGTGCAGGAAACGGTG 684  
QY 601 GAATATTTCTGTAACCTGCAATATATACCGATGCAAAACGTCATCGAGCAGGTCAGGCG 660  
Db 685 GAATATTTCTGTAACCTGCAATATATACCGATGCAAAACGTCATCGAGCAGGTAAGGCG 744  
QY 661 GTTGCATTCGAATTTGGGTTATATCACATTTTATGTTTATGTTTATGTTTATGTTTAT 720  
Db 745 GTTGCATTCGAATTTGGGTTATATCACATTTTATGTTTATGTTTATGTTTATGTTTAT 804  
QY 721 TATGCGGCTAAGGATTCGACGAGGAAAGCAATCTCTGCAAAATATAGCGTTGATTTT 780  
Db 805 TATGCGGCTAAGGATTCGACGAGGAAAGCAATCTCTGCAAAATATAGCGTTGATTTT 864  
QY 781 GATAACAAAACCAATGATGCAAGCTGATTAATAAATCAGTATGTGCGAAATATAAAGAT 840  
Db 865 GGTAAACAAAACCTGACGCGGAGCTGATTAATAAACAATATGT-----CAACCCAGT 918  
QY 841 GAACCCAAAACCAACCGCTGACATTTACGATTTACTGCAAAATTTGACGCGCAACCGCTT 900  
Db 919 GAGAACAAAACCAACCGCTGACATTTACCAATCATCATCTGCGGATTTAAACCGCAACCGCTT 978  
QY 901 ACCGCGAGTGCAGGCTCAATCTGATTTAGCGAAAAACCTTCCCGGTATAGCGGTTTG 960  
Db 979 ACCGCGAGTGCAGGCTCAATCTGATTTAGCGAAAAACCATGCCAATAAGGAGCATTTG 1038  
QY 961 TTTTCCATGCGGATCCGATCAGCGCTTGAGGCGGTTTTTTCGCGGATACGAGAA 1020



Db	1039	TTTTTCCATGCCGATGCGCATCAGCGGCTTGAGGSCGCTTTTTCCTGGCGCATGAGGGCGAA	1098
Qy	1021	GAGCTTGC CGGACGGTTTATCAGCAACGACGATTCCTGCGGCTATTCGCAAGCAAA	1080
Db	1099	GAGCTTGC CGGACGGTTTATCAGCAACGACGATTCCTGCGGCTATTCGCAAGCAAA	1158
Qy	1081	AAACAGACACAAACGACGACGATACAAACCTGCCCTCGCCCTCGGAAAAACACACC	1140
Db	1159	CA-----AAATAGCCCGTGCGCTCTGGAACACACACC	1191
Qy	1141	AAAATCTTGGATTTCTTAAAAATTTCCGTTGACGAGCGACATGATGGCCATGCCGCTAAG	1200
Db	1192	AAAATCTTGGATTTCTTAAAAATTTCCGTTGATGAGCGAAGTGCTGAAAAATCCCGCAGCG	1251
Qy	1201	TTTGCCATTTCTCTATGCCCGATTTTGTTCATCCGACAAACTTCTTGTTCGAGGGCGT	1260
Db	1252	TTTGCCATTTCTCTATGCCCGATTTTGTTCATCCGACAAACTTCTTGTTCGAGGGCGAT	1311
Qy	1261	GAAATTCCTTTGTGAACGAAGAACAAATCATCAAGCTTGC CGACGCGAGGAAAAATGACC	1320
Db	1312	GAAATTCCTTTGTGTTAGCCAGAGAAAA CCAATCGAGCTTGC CGACGCGAGGAAAAATGACC	1371
Qy	1321	GTC CGTCTGTTTGC GACTTTTGTGA CTTATGTGAATCTCGGACGATATAAAACCGATCGC	1380
Db	1372	GTCACTGCTTGTTCGCACTTTTGTGACTATGTGAACCTCGGACGATATAAAACCGAACGC	1431
Qy	1381	CCGCGAATGAAA CCAAGGCGGAAGATAAAGGGGAGATGAAAGGCTCGACGCTTGAT	1440
Db	1432	CCCGCCGCAAAACCGAAGGC-----GCAGGACGAGAGATTCGACATTTGAT	1479
Qy	1441	AACGACGAAGAAACGGAAGACGAAGCGTAGAAGACGAAGCGCGCGAGAGAACGAAACT	1500
Db	1480	AATGGCGAAGAAACGGAAGACGAATTCGGCGATGAAGAGAGAGCCACCGAGATCGAGC	1539
Qy	1501	TCCGAAAGAGGATAATGGCGAAGCGAAGAAAGCAACCGCCGAGAGAAACCGAGAGATT	1560
Db	1540	GCAGGAGATGAAGCGACGGAAGAGACGAAGCCAC-----AGAAAAAC	1581
Qy	1561	GATGAGCCGGAAGAGAGGAGATTTGAAGAACCCGAGAAAAAATCGCGCGCAGAGCAAC	1620
Db	1582	GAAACGCGGGAAGAGACGAAGCTGGAAGAACCTGAAGAGAAATTCGTCGGCAGAGGCAAC	1641
Qy	1621	GGCGTTCCAGCAGCATCTCGCTCGCTTAGAGCCCTTAAAGCGAGGACATCGACCTT	1680
Db	1642	GGCAGTTCAAAGCCATCTCTGCTGTCCCGAAGCTCTTAAGCGAGGATATCGACCTT	1701
Qy	1681	TTTCTTGAAAGGTATCCGCA CGGCAGAAACGGATATTCGCAAACCGGAAACGCGCGATTTAT	1740
Db	1702	TTTCTTGAAAGGTATCCGCA CGGCAGAAACGAAATATTCGCAAACTGGAGAGCACGCTAT	1761
Qy	1741	ACCGCATTGCGGAAGCGGTATCGGCAAAACCCATTCATTTGGGACATCAGGCGGATGAA	1800
Db	1762	ACCGGCATTGCGGAAGCGGTATCGGCAAAACCCATTCATTTGGGACATCATCGGATGAA	1821
Qy	1801	AAAGCGCAAAAGCAGAAATTTACCGTTGATTTCCACAAAGAAATCGATTTCCGGAAGCTG	1860
Db	1822	GAAAGCGCAAAAGCAGTATTTTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAACGCTG	1881
Qy	1861	ACGAGCAAAACCGCGGTAGAACCTGTTTCCATATTTGAAGACGCGCAAGATTTGATGCAAC	1920
Db	1882	ACGGAAGAAAAACGGGTAGAACCTGTTTCCGTTTGAAGAACCGCGGTGATTTGAGGGCAAC	1941
Qy	1921	GGTTTCCAGCGACAGCGCGCACTCGGAGAGCGGCATCAATCTTTTCGGGAAATGCTGTCG	1980
Db	1942	GGTTTCCATGCGACAGCGCGCACTCGGATGACGCGATCGACCTTTTCGGGACGGGTTGCG	2001
Qy	1981	ACCGACCCCAAAACATTTCCAAGCTAGTAACTCTTCGCTAGAGAGAGGATTTTACGGCCCG	2040
Db	2002	ACCAACCGCAGATCTTCAAAGCTAATGATCTTCGTTAGAGAGGAGGATTTTACGGCCCG	2061
Qy	2041	CAGCGCGCGAAATGGCGGCTACTATTTCAAATATGATGGGAAATCTCTTAGTATAACT	2100

Db	2062	AAGCGGAGGAATTGGCGGTATTATTTTCAATAATGATGGGAAATCTCTTGTGTAACCT	2122
Qy	2101	GAATAATTCAAATGAAGCTGAAGCTGAAGTTGAAGTTGAAGCTGAAGCTGAAGTTGAAG	2160
Db	2122	GAAGTACTGAATAATAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGAT	2181
Qy	2161	GTTGAAGCTGATGTTGGCAACAGTTAGAACCTGATGATGAGTTTAAACACAAATTCGGCGTG	2220
Db	2182	GCTGATGCTGATGTTG---AACAGTTAAACCCCAATTCGGCGTG	2235
Qy	2221	GTATTCGGTGGCAAGAAGATATGCAGGAGTGGMAAAATGA	2262
Db	2236	GTATTCGGTGGCAAGAAGATATAAAGAGGTGGMAAAATGA	2277
RESULT 8			
LOCUS	BD074755	2277 bp	DNA linear
DEFINITION	Neisseria lactoferrin-binding protein.		
ACCESSION	BD074755		
VERSION	BD074755.1	GI:22620358	
KEYWORDS	JP 2001514894-A/1.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 2277)		
AUTHORS	Felnhelm,A.M.P. and Thomsen,J.P.M.		
TITLE	Neisseria lactoferrin-binding protein.		
JOURNAL	Patent: JP 2001514894-A 1 18-SEP-2001.		
COMMENT	UNIVERSITY OF UTRERECHT, TECHNOLOGY FOUNDATION		
	OS Unidentified		
	PN JP 2001514894-A/1		
	PD 18-SRP-2001		
	PF 10-AUG-1998 JP 2000509840		
	PR 15-AUG-1997 GB 9717423.9 05-FEB-1998 GB 9802544.8 PI		
	ANICA MARGARETA PETERSON FELNHOLM, JOHANNES PETRUS MARIA PI THOMSEN		
	PC C12N15/09,A61K39/095,A61K39/395,A61K48/00,A61P31/12,C07K14/12,C07K14/22		
	PC C07K16/12,		
	PC C12N1/21,C12P21/02,C12P21/08,G01N33/15,G01N33/50,G01N33/68,P01N33/68		
	C12N15/00		
	CC Strandedness: Double;		
	CC Topology: Linear;		
	CC Neisseria lactoferrin-binding protein		
	EH Key	Location/Qualifiers	
	FT source	1..2277	
	FT	/organism='Unidentified'.	
FEATURES			
	source	Location/Qualifiers	
		1..2277	
		/organism="unidentified"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:32644"	
ORIGIN			
	Query Match	64.8%;	Score 1465.2; DB 6; Length 2277;
	Best Local Similarity	81.1%;	Pred. No. 2.5e-304;
	Matches 1835;	Conservative	0; Mismatches 343; Indels 84; Gaps
Qy	1	ATGTGTAACCGAATTAATGGCGGCAATGTTGTTGCCCTTACTTGTAGCATCTTGTATC	60
Db	100	ATGTGTAACCGAATTAATGGCGGCAATGTTGTTGCCCTTACTTGTAGCATCTTGTATC	159
Qy	61	GGCGGCAATTTCCGGGTGACAGCTGTTGTCGAATCAACGCCGACCGCGCAACTCTGTCA	120
Db	160	GGCGGCAATTTCCGGGTGACAGCTGTTGTCGAATCAACGCCGACCGCGCGG	207
Qy	121	GATTTCCAAATCTTCCAAATCTCGGATAAGCCCTGTCAGCTCCTGCCGAGCCCTTCGTA	180
Db	208	TACCCGCTCACTTTCAAGTCTAAGGACGTTCCCACTCCGCCCTCGCAACCTTCTATA	267
Qy	181	GAATACAGCGGTCATAGCGGCGCGGTCGGTCCGCAATCGGCTGCCAAGCGCAAT	240
Db	268	GAATACAGCGGTCATAGCGGCGCGGTCGGTCCGCAATCGGCTGCCAAGCGCAAT	327

Qy	241	ATCGCAACTTTTGATAAAAATGGTAATGAAATTCCTCCAAATAGTAAAGCAGCGAGGGTAT	300
Db	328	ACTGCTTTTCATCGTGAAGATGCGACGGAATTCGAATAGCMAACAGCAGAGAAAG	387
Qy	301	CTGCCGCTCAAGAGAGAGATATCCTGTGTTTTTATAGCGGTACGCGGAAAGAACAGGCTGAC	360
Db	388	CTGTGTTTTCAAGAAGGTGATGTTCTGTGTTTTTATACGGTTCAAAAGGAATTAACCTTCAA	447
Qy	361	AAACTTTAAAAAGGAATCAACGACGGCATCCTAATGCAACCAATCTACAGTCCGATTTA	420
Db	448	CAACTTTAAAGCGAAATCATTAACGTGAATCCGATGTAGAAATTAGGACATCAGAAAG	507
Qy	421	AAAGATGATGCGGTATCAATATAAATATGTCCGGCCGGATATGTTTTATCTAGATATCGA	480
Db	508	GAAAAATAAAAAATATGATTATAAATTTGTAGATGAGGTTATGTATA---TGTAAGGGA	564
Qy	481	ACAGATGAATCGAACGAACCTCAGCGGTAAGCGGTTACCCACCGTTAGGTTATGAC	540
Db	565	AAAGATGAATAATTAAGTGGAATTCAGATTACAAGCAGTTTCCAACCGTTAGGTTATGAC	624
Qy	541	GGTTTTGTATATATTTCCGCGAAGCTCTTCCCAATCTTTACCGAGTCGGGAAACGGTG	600
Db	625	GGTTTTGTATATATTTCCGAGAGCTCTTCCCAATCTTTACCGAGTCGGGAAACGGTG	684
Qy	601	GAATATCTGTGTAACTGGCAATATATGACCGATGCCAAGCTCATCGACAGGTTCAGCG	660
Db	685	GAATATCTGTGTAACTGGCAATATATGACCGATGCCAAGCTCATCGACAGGTTAAGCG	744
Qy	661	GTTCGCATTGCAATTTGGTTATATCAATTTTANGTAAACGATGTTGGTCAACTTCT	720
Db	745	GTTCGCATTGCAATTTGGTTATATCAATTTTATGGTAAACGATGTTGGTCAACTTCT	804
Qy	721	TATCGCGCTAAGGATGTCGACGAAGGGAAGAGCATCTGCGCAATATACGGTTGATTT	780
Db	805	TATCGCGCTAAGGATGTCGACGAAGGGAAGAGCATCTGCGCAATATACGGTTGATTT	864
Qy	781	GATTAACAAAACCATGAATGGCAAGCTGATTAATAATCAGTATGTGCGAAATATAAAAAAGAT	840
Db	865	GGTAACAAAACCCCTGACGGCGAGCTGATTAATAAACCAATATGT-----CAAAACCCAGT	918
Qy	841	GAAACCAAAAACCGCTGACCAATTTACGACATTAACGAAATTTGGACGCAACCGCTTT	900
Db	919	GAGAAGCAAAAACCGCTGACCAATTTACGACATTAACGAAATTTGGACGCAACCGCTTT	978
Qy	901	ACCGCAGTGCACAAGGTCAATCTCGATTTAGCGAABAAACCTTCGCGGTATAGCGTTG	960
Db	979	ACCGCAGTGCACAAGGTCAATCTCGATTTAGCGAABAAACCTTCGCGGTATAGCGTTG	1038
Qy	961	TTTTTTCATGCGCATGCGATCAGCGCTTTGAGGGCGGTTTTTTTTCGGCGAATAACGGAGAA	1020
Db	1039	TTTTTTCATGCGCATGCGATCAGCGCTTTGAGGGCGGTTTTTTTTCGGCGAATAAGGGGAA	1098
Qy	1021	GAGCTTCGGGACGGTTTATACGAAACGACAAACAGCGTATTCGGCGTATTCGAGGCAAA	1080
Db	1099	GAGCTTCGGGACGGTTTATACGAAACGACAAACAGCGTATTCGGCGTATTCGAGGCAAA	1158
Qy	1081	AAAAACAGACAGCAAAACGACGAGATACAAAACCTTCCTTCGGCTCGGAAACACACC	1140
Db	1159	CA-----AAATAGCCCGTGCCTGCTGAAACACACC	1191
Qy	1141	AAATCTTGATTTCTCTAAAAATTCGGTTGACAGGCGCATGATGCCATGCCCGTAAG	1200
Db	1192	AAATCTTGATTTCTCTGAAAAATTCGGTTGATGAGGCAAGTGTGAAATCCCCGACCG	1251
Qy	1201	TTTGCCATTTCTCTATGCCCCGATTTTGGTTCATCCGCAAACTCTTCTGTGAAAGGGCT	1260
Db	1252	TTTGCCATTTCTCTATGCCCCGATTTTGGTTCATCCGCAAACTCTTCTGTGAAAGGGCAT	1311
Qy	1261	GAAATTCCTTTGGTAAACGAAGAAACAAATCATCAAGCTTCGCGACGGCAGGAATGACC	1320
Db	1312	GAAATTCCTTTGGTAGCCAGAGAAACCATCGAGCTTCGCGACGGCAGGAATGACC	1371

RESULT 9	ACCESSION
AF049349	VERSION
LOCUS	
DEFINITION	



Db 941 CAACTTAAAGCGAAATTCATAAACGCTGATTCCTGATGTAGAAATAGACATCAGAAAG 1000  
Qy 421 AAACATGATGGTATCAATATAAATATGTTCGGGCGGATGATGTTTATCTAGATATGGA 480  
Db 1001 GAAATTAATAAATATGATTAATAAATTTGTAGATCAGGTTATGTATA---TGTAAGGGA 1057  
Qy 481 ACAGATGAAATCGAACAGAACTCAGGGGGTAAAGCGGTTACCCACCGCTTAGGTTATGAC 540  
Db 1058 AAAGATGAAATTAAGTGGACTTCAGATTACAGCAGTTTTCCAAACCGCTTAGGTTATGAC 1117  
Qy 541 GGTTTTGTATATATTCGGAGAAAGTCCTTCCCAATCTTTTACCGAGTGGGGAACGGTG 600  
Db 1118 GGTTTTGTATATATTCGGAGAAAGTCCTTCCCAATCTTTTACCGAGTGGGGAACGGTG 1177  
Qy 601 GAATATTTCTGGTAACTCGCAATATATACCGATGTCGCAAAAGTCATCAGAGAGTCAAGCG 660  
Db 1178 GAATATTTCTGGTAACTCGCAATATATACCGATGTCGCAAAAGTCATCAGAGAGTCAAGCG 1237  
Qy 661 GTTGGCATTCACAAATTTGGGTTATATCACATTTTATGTTAAACGATGTTGTTGCACTTCT 720  
Db 1238 GTTGGCATTCACAAATTTGGGTTATATCACATTTTATGTTAAACGATGTTGTTGCACTTCT 1297  
Qy 721 TATCGGCTTAAGATGTGACGAAAGGAAAGCATCTCTGCAAAATATACGTTGATTTT 780  
Db 1298 TATCGGCTTAAGATGTGACGAAAGGAAAGCATCTCTGCAAAATATACGTTGATTTT 1357  
Qy 781 GATAACAAACCATGAATGCGAGCTGATTAATAATTCAGTATGCGAAATATAAAGAT 840  
Db 1358 GGTAAACAAACCATGAATGCGAGCTGATTAATAATTCAGTATGCGAAATATAAAGAT 1411  
Qy 841 GAAACCAAAACCATGACCAATTTACGACATTTACTGCAAAATTTGACGCGCAACCGCTTT 900  
Db 1412 GAAACCAAAACCATGACCAATTTACTGCAAAATTTGACGCGCAACCGCTTT 1471  
Qy 901 ACCGCGAGTGCAGAGTCAATCTGATTTAGCGAAAGCATGTCGCAATAGGCGATTG 960  
Db 1472 ACCGCGAGTGCAGAGTCAATCTGATTTAGCGAAAGCATGTCGCAATAGGCGATTG 1531  
Qy 961 TTTTTCATGCGGATCGCGATCAGCGCTTGAGGCGGTTTTTTTCGCGCATACGAGGAA 1020  
Db 1532 TTTTTCATGCGGATCGCGATCAGCGCTTGAGGCGGTTTTTTTCGCGCATACGAGGAA 1591  
Qy 1021 GAGCTTGGCGGAGGTTTTATCAGCAACAGACAGCTATTCGCGGTTATTCGAGGCAAA 1080  
Db 1592 GAGCTTGGCGGAGGTTTTATCAGCAACAGACAGCTATTCGCGGTTATTCGAGGCAAA 1651  
Qy 1081 AAAACAGAGACAGCAACAGCAGATACAAACCTGCCCTGCGCTCGGAAACACACACC 1140  
Db 1652 CA-----AAATAGCCCGTGCGCTCTGGAAACACACACC 1684  
Qy 1141 AAAATCTTGGATTTCTATAAATTTCCGTTGACGAGGCGACTGATGGCCATGCGCGTAAG 1200  
Db 1685 ABAATCTTGGATTTCTGAAAATTTCCGTTGATGAGGCAAGTGTGAAATATCCCGACCG 1744  
Qy 1201 TTTGCGATTTCTCTATGCGCGATTTTGGTCAATCCGCAAACTTCTTGTGCAAGGGCGT 1260  
Db 1745 TTTGCGATTTCTCTATGCGCGATTTTGGTCAATCCGCAAACTTCTTGTGCAAGGGCGAT 1804  
Qy 1261 GAAATCTTTTGGTAAACGAGAAACAATCATCAAGCTTGCAGCGGAGGAAATGACC 1320  
Db 1805 GAAATCTTTTGGTAAACGAGAAACAATCATCAAGCTTGCAGCGGAGGAAATGACC 1864  
Qy 1321 GTCCGCTCTTCTGCGACTTTTTCACCTATCTGAACTCGACGAGATGAAGGGTGCAGGCTGC 1380  
Db 1865 GTGAGTCTTCTGCGACTTTTTCACCTATCTGAACTCGACGAGATGAAGGGTGCAGGCTGC 1924  
Qy 1381 CCGCAAGTAAACCAAGCGGAGAGATAAAGGCGAGGATGAAGGGTGCAGGCTGCAGGCTGC 1440  
Db 1925 CCGCGCCAAACCGAAGGCG-----GCAGGACGAGAGGATTCGACATTTGAT 1972  
Qy 1441 AACGACGAGAGCGAAGCGAAGCGGTAGAACGAGCGCGCGAGGAGAGCAAACT 1500

Db 1973 AATGGCGAAGAAACGGAAGACGAATAATCGCGCATGAAGAAGAGGACCGCAAGATCGACCC 2032  
Qy 1501 TCCGAAGAGGATATATGCGAAGACGGAAGACCAACCCGCCGGAAGAAACCGCAAGAACTT 1560  
Db 2033 GCAGGAGATGAGGCGACGGAAGAGACGAAGCCAC-----AGAAAC 2074  
Qy 1561 GATGAACCCGAAGAGGAGGAGGTTGAAGAACCAGAAATAATCGCGGAGAGGAGCAAC 1620  
Db 2075 GAAGACGCGGAAGAGAGAGAGCTGAAGAACCTGAAGAGANTCTCGCGCAAGAGGCAAC 2134  
Qy 1621 GCGGTTACGCGAGCATCTCTGCTGCTTGAAGAGCTCTTAAAGCGAGGGAATCGACCTT 1680  
Db 2135 GCGAGTTCAAACGCCCATCTCTGCTGCTTCCGGAAGCTCTTAAAGCGAGGATATCGACCTT 2194  
Qy 1681 TTCTCTGAAAGGTTATCGCACGCGAGAAACGATATTTCCGCAAAAGCGGCAATCATAT 1740  
Db 2195 TTCTCTGAAAGGTTATCGCACGCGAGAAACGAAATTTCCGCAAACTCGAGAGCACGCTAT 2254  
Qy 1741 ACCGCGACTTGGGAAGCGGCTATCGGCAAAACCATTTCAATGGGCAATCATAGGCGGATGA 1800  
Db 2255 ACCGCGACTTGGGAAGCGGCTATCGGCAAAACCATTTCAATGGGCAATCATAGGCGGATGA 2314  
Qy 1801 AAGCGGCAAAAGCAGATTTACCGTTGATTTTCGAACAAGAAATCGATTTCCGGAAGCTG 1860  
Db 2315 GAAGCGGCAAAAGCAGATTTACCGTTGATTTTCGGAAGAAATCGATTTCCGGAAGCTG 2374  
Qy 1861 ACGGAGCAAAACCGGCTAGAACCTGCTTTCCATATTTGAAGCGGCAAGATTTGATGCAAC 1920  
Db 2375 ACGGAGCAAAACCGGCTAGAACCTGCTTTCCATATTTGAAGCGGCTGATTTGAGGCAAC 2434  
Qy 1921 GGTTTCCACGCGACGCGGCTATCGGAGAGCGGCTCAATCTTTCCGGAATGCTTCG 1980  
Db 2435 GGTTTCCATGCGACAGCGGCTATCGGAGTGAAGCGGCTGATTTCCGGAAGCTTCG 2494  
Qy 1981 ACCGACCCCAACATTCGAGCTAGTAAATCTTCGTTGAGAGAGGAGATTTTACGCGCG 2040  
Db 2495 ACCAACCCGAGATCTTCAAGCTAATGATCTTCGTTGAGAGAGGAGATTTTACGCGCG 2554  
Qy 2041 CAGGCGCGGGAATTCGCGGCTACTATTTTCAATATGATGGGAATCTCTAGTAACT 2100  
Db 2555 AAGCGGAGGATTTGCGCGGTTATTTTCAATATGATGGGAATCTCTAGTAACT 2614  
Qy 2101 GAAATATTTGAATAAGCTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 2160  
Db 2615 GAAAGTACTGAAATATAAGTTGAAGCTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 2674  
Qy 2161 GTTGAAGCTGATTTGGCAACAGTTGAACCTGATGAAGTTAAACACAAATTTCCGCGTG 2220  
Db 2675 GCTGATGCTGATGTTG---AACAGTTAAACCC---TGAAGTTAAACCCCAATTCGCGTG 2728  
Qy 2221 GTATTCGCGTGCAGAAAGATATGACGAGGCTGGAAATGCA 2262  
Db 2729 GTATTCGCGTGCAGAAAGATATTAAGAGGTGGAAATGCA 2770

## RESULT 10

AF031432

LOCUS

DEFINITION

Neisseria meningitidis

precursor (lbpB) gene, complete cds.

AF031432

VERSION

AF031432.1

GI:3213214

SOURCE

ORGANISM

Neisseria meningitidis

Neisseria meningitidis

Bacteria; Proteobacteria;

Neisseriaceae; Neisseria.

1 (bases 1 to 2537)

Bonnah, R.A. and Schryvers, A.B.

Preparation and characterization of Neisseria meningitidis mutants

deficient in production of the human lactoferrin-binding proteins

lbpA and lbpB

J. Bacteriol. 180 (12), 3080-3090 (1998)

AF031432 2537 bp DNA linear BCT 12-JUN-1998

Neisseria meningitidis B16b6 lactoferrin binding protein B

precursor (lbpB) gene, complete cds.

AF031432

AF031432.1 GI:3213214

Neisseria meningitidis

Neisseria meningitidis

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria.

1 (bases 1 to 2537)

Bonnah, R.A. and Schryvers, A.B.

Preparation and characterization of Neisseria meningitidis mutants

deficient in production of the human lactoferrin-binding proteins

lbpA and lbpB

J. Bacteriol. 180 (12), 3080-3090 (1998)



Db	1572	GAATTCCTTTGGTTAGCCACGAGAAAAACCATCGAGCTTGCCGACGGCAGGAAAAATGACC	1631
QY	1321	GTCCGTGCTTGTTCGGACTTTTTTGACCTATGTGAAACTCGACCGGATAAAACCGATCGC	1380
Db	1632	GTCACTGCTTGTTCGGACTTTTTTGACCTATGTGAACTTCGGACCGGATAAAACCGAACGT	1691
QY	1381	CCGGCAAGTAAACCAAAGCGGAGATAAAGGGGAGGATGAAGAGGTGTCAGGCGTTGAT	1440
Db	1692	CCCGCGCCCAACCGAAGGC-----GCAGGACGAAGAGGATTCGGACATTGAT	1739
QY	1441	AACGACGAAGAAGCGAAGACGAGCCGTAGAAACGACGAGCGCGGAAGAGAGCAAACT	1500
Db	1740	AATGCGGAGAAAGCGAAGAAGAAATCGGCATGAAGAAGAAGCACCGAAGATGCAGCC	1799
QY	1501	TCCGAAGAGGATTAATGGCGAAGACGAAGAAGCAACCGCGAAGAAGAAACCGAAGAGATT	1560
Db	1800	GCAGGAGATGAAGGCGAGCGAAGACGAAGCCAC-----AGAAAC	1841
QY	1561	GATGAAGCCGAGAGGAGGAAGTTGAAGAACCGGAAGAAAATTCGCGGACGAAGGCAAC	1620
Db	1842	GAAGACGCGAAGAGACGAAGCTGAAGAACCTGAAGAAGATCGTCGGCAGAAGGCAC	1901
QY	1621	GCGCGTTCAAGGAGCATCTCTCCCTCGCTTAAAGGCTCTTAAGGCGAGGATATCGACCTT	1680
Db	1902	GCGAGTTCAAGGCGCATCTCTCCCTCGCGAAGCCTTAAGGCGAGGATATCGACCTT	1961
QY	1681	TTCTGTAAGGTATCCGACGCGCAGAAACCGATATTCGCAAGACGGAACGGCGCATTA	1740
Db	1962	TTCTGTAAGGTATCCGACGCGCAGAAACGAAATATTCGCAAACTGGAGNAGCACGCTAT	2021
QY	1741	ACCGGCACTTGGGAAGCGGTATCGGCAAAACCCATTAATGGGACAAATCAGCGGATGAA	1800
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[illegible]







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ACCESSION  
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VERSION  
AF123380.1 GI:4884686

2226 bp DNA linear BCT 24-MAY-1999  
Neisseria meningitidis strain H44/76 lactoferrin-binding protein  
precursor (lbpB) gene, complete cds.  
AF123380  
AF123380.1 GI:4884686

KEYWORDS

SOURCE Neisseria meningitidis  
ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.

REFERENCE 1 (bases 1 to 2226)  
AUTHORS Pattersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tomassen,J.

TITLE Sequence variability of the meningococcal lactoferrin-binding

protein lbpB

JOURNAL Gene 231 (1-2), 105-110 (1999)

MEDLINE 99250255

PUBMED 10231574

REFERENCE 2 (bases 1 to 2226)  
AUTHORS Pattersson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tomassen,J.

TITLE Direct Submission

JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology,

Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands

FEATURES

source

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ORIGIN

Query Match 63.8%; Score 1442.2; DB 1; Length 2226;  
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			Bacteria; Proteobacteriia		
			Neisseriaceae; Neisseria.		
	REFERENCE		1 (bases 1 to 2226)		

AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
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Pettersson-Fernholm, A.M. and Tommassen, J.P.  
NEISSERIA LACTOFERRIN BINDING PROTEIN  
Patent: WO 990176-A 5 25-FEB-1999;  
UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIKA MAR (NL)

source

Location/Qualifiers  
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**CDS**

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## ORIGIN

Query Match	63.8%;	Score 1442.2;	DB 6;	Length 2226;
Best Local Similarity	80.3%;	Pred. No. 2.2e-299;		
Matches 1828:	Concentrations	Amino acids		

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Db 1426 GCGGTTGTTGTAACGAGAGAGGACGAGAGATGAGCCGACGAGAGGACGAGAGGCG 1485  
QY 1489 GAAGACGAATCTTCGAGAGGATTAATGGCGAAGACGAGAAACCGCGGAGAGAA 1548  
Db 1486 GAAGACGAATCTTCGAGAGGATTAATGGCGAAGAGGAGTTCGAGAAACGAGAGC 1536  
QY 1549 ACCGAGAGTTGATGAGCGGAGAGGAGGATTTGAAGAACCCGAGAGAAATCCCG 1608  
Db 1537 AACGAGCGCGGAGAGAGAGAGCTGTAAGAACCTGAGAGACCGAGAGAGATCCCG 1596  
QY 1609 GCAGAGGCAAC---GGCGGTTTACGCGAGCATCTGCTGCTCTGAGAGCTCTAAAGGC 1665

Db 1597 GCAGAGCGCGGTGGTGGTTTCAGACGGCATCTGCGCGCTCCGAGAGCTCTTAAAGGC 1656  
QY 1666 AGGACATCGACCTTTTCTTGAAGGTATCCGACGCGCAGAAACGGATATTTCCGCAAGC 1725  
Db 1657 AGGATATCGACCTTTTCTTGAAGGTATCCGACGCGCGGAGCGCATTTCCGCAACT 1716  
QY 1726 GGAACGCGCATTTATACCGGCACTTGGGAGCGGTATCGGCAAAACCCATTTCAATGGAC 1785  
Db 1717 GGAAGACGCGTATACCGGCACTTGGGAGCGGTATCAGCAAAACCCATTTCAATGGAC 1776  
QY 1786 AATCAGCGGATGAAAAAGCGGCAAAAGCAGAAATTTACCGTTGATTTCGACAGAAATCG 1845  
Db 1777 AATCATGCGGATAAAAAAGCGGCAAAAGCAGAAATTTGACGTTGATTTCGCGGAGAAATCG 1836  
QY 1846 ATTTCCGGAAGCTTGACGAGCAAAACGCGCTGAGAACTGTTTCCATATTTGAAGACGCG 1905  
Db 1837 ATTTCCGGAACGCTGACGAGCAAAACGCGTGTACAACTGTTTCCATATTTGAAGACGCG 1896  
QY 1906 AAGATTGATGCAACCGTTTCCAGCGACAGCGCGCACTCGGAGAGCGGCATCAATCTT 1965  
Db 1897 GTGATTGAGGCAATGTTTCCACGCGACAGCGCGCACTCGGATTAACGGCATCAATCTT 1956  
QY 1966 TCGGAAATGTTTCGACCGCAACCCAAACATTTCCAGCTAGTAACTTTCTGTTAGAGGA 2025  
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RESULT 14  
BD074757

LOCUS BD074757 2226 bp DNA linear PAT 27-AUG-2002  
DEFINITION Neisseria lactoferrin-binding protein.  
ACCESSION BD074757  
VERSION BD074757.1 GI:22620360  
KEYWORDS JP 2001514894-A/3.  
SOURCE unidentified  
ORGANISM Neisseria lactoferrin-binding protein.  
REFERENCE 1 (bases 1 to 2226)  
AUTHORS Felnholm, A.M.P. and Thomsen, J.P.M.  
TITLE Neisseria lactoferrin-binding protein  
JOURNAL Patent: JP 2001514894-A 3 18-SEP-2001;  
UNIVERSITY OF UTRICHT, TECHNOLOGY FOUNDATION  
COMMENT OS Unidentified  
EN JP 2001514894-A/3  
PD 18-SEP-2001  
PF 10-AUG-1998 JP 2000509840  
PR 15-AUG-1997 GB 9717423.9, 05-FEB-1998 GB 9802544.8 PI  
ANICA MARGARETA PETERSON FELNHOLM, JOHANES PETRUS MARIA PI  
THOMSEN  
PC C12N15/09, A61K39/095, A61K39/395, A61K48/00, A61P31/12, C07K14/22,  
C07K16/12,  
PC C12N1/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC  
C12N15/00  
CC Strandedness: Double;  
CC Topology: Linear;  
CC Neisseria lactoferrin-binding protein

FEATURES		FH	Key	Location/Qualifiers	FT
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		FT	source	1..2226	/mol_type='genomic DNA'
		FT	source	/db_xref='taxon:32644'	
ORIGIN					
Query Match					
Best Local Similarity 63.8%; Score 1442.2; DB 6; Length 2226;					
Matches 1828; Conservative 0; Mismatches 383; Indels 66; Gaps 9;					
QY	1	ATGTGTAACCGCAATTATGCGGCATTTGCTCTTGGCCCTTACTTTTAGCATCTTGTATC	60		
Db	1	ATGTGTAACCGCAATTATGCGGCATTTGCTCTTGGCCCTTACTTTTGGCATCTGTATT	60		
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Db	61	GCGCGCAATTTCCGGGTGACGCTGTTGTCGAATCAACGCGCACCGCG-----	108		
QY	121	GATTCCAATCTTCCAAATCTGCGGATAAGCCTGCTCCAGCTCCTCCGAGCCTTCGGTA	180		
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QY	181	GAATCAACGCGGT-----CAAGCGGCCCGCTCGGTGCGGCAATGCGGCTGCCAAGG	234		
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Db	229	CGGAATTTCCCAACTTCTGATAAGGTTGGCAATGATTTTCCAAATAGCAAAACAGCAHA	288		
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Db	289	GAAGAGCTGCTGTTTAAAGAGGATGATGTTCTGTGTTTATACGGTTCAAAAAAGATAA	348		
QY	355	GCTGCAAACTTAAAGAGAAATCAACGCGCGCATCTTAATGACCAATCTTACAGTCC	414		
Db	349	CTTCAGTGGCTTAGGATAAAATTCATCAACGCAATCTTAATGTAGAAATTAGGACATCA	408		
QY	415	GATTTAAAGATGATGGTATCAATATAATATGTCGCGGCGGATATGTTTATACTAGA	474		
Db	409	GAATATGAATAAATAATATGTTATGAAATTTGTGATGCCGCTTATGTATATCTAAA	468		
QY	475	TATGGAACAGATGAATTCGAACAGAACTCAGCGGTTAAGCGGTTACCCCGCTTAGGT	534		
Db	469	AACGGAACAGATGAATTTGCTGGACCTTCAAAATCGCAAGCAGTTTCTAATCGTTTGGC	528		
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QY	1012	AACGGAAGAGCTTCCCGACCGTTTATCAGCAACGACAAACGCGTATTCGGCGTATTC	1071		
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QY	1312	AAAAATGACGCTGCTGTTGTTGCACTTTTGTGAACTATGTGAAACTCGAGCGATATAA	1371		
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Db	1366	ACTGACCGCCCGCAAGTAAACCAAGCGGAGAGATTAAGGGAGAGATGAAGAGGTATCA	1425		
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QY 721 TATGCGGTAAAGGATGTCGACGAAGGGAAGGATCCTGCGCAAAATATACGGTTGATTTT 780  
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QY 1018 TATGCGGTAAAGGATGTCGACGAAGGGAAGGATCCTGCGCAAAATATACGGTTGATTTT 1077  
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QY 781 GATAACAAACCATGAATGCGAAGCTGATTAATAAATCAGTATGTGCGAAATATAAAGAT 840  
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QY 841 GAACCCAAAACCGCTGACCATTTACGACATTAATGCAAAATTTGACCGCAACCGCTTT 900  
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QY 1618 AACGGCGTTCAGGCAGCATCTGCTGCCCTAGAAAGCTCTAAAGGCGAGGACATCGAC 1677  
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QY 1678 CTTTTCCTGAAAGGTATCCGACGCGAGAAACGGATATTCGCAAGCGGAACGCGCAT 1737  
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QY 2014 TATACCGGCTTGGGAAGCGGATTCGGCAAAACCCATTCATGGAACAATCAGCGGAT 2073  
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QY 1798 GAAAAACGGCAACGAGAAATTTACCGTTGATTTGCAAGAAATCGATTTCCGGAAG 1857  
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QY 2395 GAAATGAAGCTGATGTTGGCGAACAGTTAGAAC---TGAAGTTAAACCCCAATTCGCG 2451  
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QY 2218 GTGGTATTTCGGTCCGAAGAAAGATATGAGGAGGTGGAAAAATGA 2262  
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Search completed: August 24, 2004, 23:47:47  
Job time : 8501.05 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:48:44 ; Search time 766.365 Seconds  
(without alignments)  
12538.967 Million cell updates/sec

Title: US-10-735-098-7  
Perfect score: 2262  
Sequence: 1 atgtgtaaacgaattatgg.....tcagaggaggtggaataatga 2262

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2262	100.0	2262	2 AAX23322	Aax23322 N. mening
2	1558	68.9	110000	3 AA81489_1	Continuation (2 of
3	1558	68.9	349980	3 AAF21611	Aaf21611 Neisseria
4	1465.2	64.8	2277	2 AAX23319	Aax23319 N. mening
5	1442.6	63.8	2226	7 ACA11945	Aca11945 Prokaryot
6	1442.2	63.8	2226	2 AAX23321	Aax23321 N. mening
7	1291.8	57.1	2124	2 AAX23323	Aax23323 N. mening
8	1250.6	55.3	2169	2 AAX23320	Aax23320 N. mening
9	1100.2	48.6	14652	3 AA81482	Aa81482 N. mening
10	730	32.3	1000	4 AAF91389	Aaf91389 N. mening
11	730	32.3	1000	6 ABK37769	Abk37769 DNA seque
12	455.6	20.1	707	3 AA81815	Aa81815 N. mening
13	169.2	7.5	3300	6 AAS67377	Aas67377 Neisseria
14	102	4.5	963	5 AAS68580	Aas68580 DNA encod
15	99.2	4.4	400	5 AAS75460	Aas75460 DNA encod
16	95.4	4.2	708	5 AAS69547	Aas69547 DNA encod
17	95.4	4.2	708	5 AAS75461	Aas75461 DNA encod
18	95.2	4.2	372	5 AAS75452	Aas75452 DNA encod
19	95.2	4.2	1072	5 AAS90738	Aas90738 DNA encod
20	95	4.2	801	5 AAS90729	Aas90729 DNA encod
21	94.2	4.2	29392	2 AAV15422	Aav15422 Mouse pol
22	93.4	4.1	379	5 AAS90909	Aas90909 DNA encod
23	93.4	4.1	379	5 AAS75428	Aas75428 DNA encod

24	93.4	4.1	379	9 ADE09716	Ade09716 Novel DNA
25	93.2	4.1	49999	2 AAZ23896	Aaz23896 Murine LO
26	93.2	4.1	49999	2 AAZ23891	Aaz23891 Murine LO
c	93	4.1	453	5 AAS92079	Aas92079 DNA encod
28	93	4.1	510	5 AAS90687	Aas90687 DNA encod
29	93	4.1	510	5 AAS69539	Aas69539 DNA encod
30	93	4.1	510	5 AAS71141	Aas71141 DNA encod
31	92.8	4.1	309	5 AAS71089	Aas71089 DNA encod
32	92	4.1	1686	2 AAQ87587	Aaq87587 DNA encod
33	91.6	4.0	96596	8 ADA02564	Ada02564 Human RAS
34	91.6	4.0	96596	2 ADB72302	Adb72302 Human RAS
35	91.4	4.0	2334	9 AAS90705	Aas90705 DNA encod
36	90	4.0	248	5 AAS90707	Aas90707 DNA encod
c	90	4.0	305	4 AAI21797	Aai21797 Probe #11
38	90	4.0	305	4 ABA66871	Ab66871 Human foe
c	90	4.0	305	4 AAI47083	Aai47083 Probe #15
c	90	4.0	305	4 ABA48950	Ab48950 Human bre
c	90	4.0	305	4 ABA33942	Ab33942 Probe #12
c	90	4.0	305	4 AAK41027	Aak41027 Human bon
c	90	4.0	305	4 AAK15306	Aak15306 Human bra
c	90	4.0	305	4 ABS40624	Ab40624 Human liv
c	90	4.0	305	5 AAI07480	Aai07480 Probe #74

ALIGNMENTS

RESULT 1  
AAX23322  
ID AAX23322 standard; cDNA; 2262 BP.  
XX  
AC AAX23322;  
XX  
DT 11-JUN-1999 (first entry)  
DE N. meningitidis strain M990 LbpB cDNA.  
XX  
KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;  
KW meningitis; diagnosis; treatment; ds.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2262  
FT /\*tag= a  
FT /product= "LbpB"  
XX  
PN WO9909176-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 10-AUG-1998; 98WO-EP005117.  
XX  
PR 15-AUG-1997; 97GB-00017423.  
PR 03-FEB-1998; 98GB-00002544.  
XX  
PA (UYU- ) RIJKSUNIV UTRECHT.  
PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.  
XX  
PI Pettersson-Fernholm AM, Tommassen JPM;  
XX  
DR WPI; 1999-190165/16.  
DR P-PSDB; AAW93495.  
XX  
XX New lactoferrin-binding protein B polynucleotides - obtained from  
XX Neisseria meningitidis, used to develop products for the diagnosis,  
XX prevention and treatment of neisserial disease, e.g. meningitis.  
PS Claim 2; Page 98-102; 116pp; English.  
XX  
XX This invention describes novel lactoferrin-binding protein B (LbpB)  
XX strains of Neisseria meningitidis. The products of this invention can be  
XX used for vaccinating humans against neisserial disease e.g. meningitis.  
CC

*applied*

CC Antibodies raised against the proteins of the invention can be used for  
 CC diagnosing or treating neisserial disease in humans. The lbpB  
 CC polypeptides can also be used for identifying compounds which inhibit the  
 CC polypeptides  
 XX  
 SQ Sequence 2262 BP; 698 A; 487 C; 590 G; 487 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 2262; DB 2; Length 2262;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGTGTAACCGAATATGCGGCATCTCTGTGTCCTTACCTTTAGCATCTGTATC 60  
 DB 1 ATGTGTAACCGAATATGCGGCATCTCTGTGTCCTTACCTTTAGCATCTGTATC 60  
 QY 61 GCGGCAATTTGCGCGTACAGCCTGTGTGCAATCAACGCGCAGCGCCCAACTCTGTCA 120  
 DB 61 GCGGCAATTTGCGCGTACAGCCTGTGTGCAATCAACGCGCAGCGCCCAACTCTGTCA 120  
 QY 121 GATTCCAAATCTTCAATCTCGGATAGAGCTGTCTCAGCTCTCGAGCCTCTCGTA 180  
 DB 121 GATTCCAAATCTTCAATCTCGGATAGAGCTGTCTCAGCTCTCGAGCCTCTCGTA 180  
 QY 181 GAAATCAGCGCGTCAAGCGCCCGCGTGGTGGCAATGCGGCTGCCAAGCGGAAT 240  
 DB 181 GAAATCAGCGCGTCAAGCGCCCGCGTGGTGGCAATGCGGCTGCCAAGCGGAAT 240  
 QY 241 ATCGCAATCTTTGATAAAATGTAATGAAATCCCAATAGTACGAGCGAGAGPAT 300  
 DB 241 ATCGCAATCTTTGATAAAATGTAATGAAATCCCAATAGTACGAGCGAGAGPAT 300  
 QY 301 CTGCGCTCAAGAGAGGATATCTGTTTATAGCGTACCGGTAAGCAAGAGCTGAC 360  
 DB 301 CTGCGCTCAAGAGAGGATATCTGTTTATAGCGTACCGGTAAGCAAGAGCTGAC 360  
 QY 361 AAACCTTAAAGAGAAATCAACGCGCATCTTAATGACCAATCTACACGCTCCGATTA 420  
 DB 361 AAACCTTAAAGAGAAATCAACGCGCATCTTAATGACCAATCTACACGCTCCGATTA 420  
 QY 421 AAAGATGATGCTATCAATATAAATATATGTCGGGCGGATATGTTTATAGTATGGA 480  
 DB 421 AAAGATGATGCTATCAATATAAATATATGTCGGGCGGATATGTTTATAGTATGGA 480  
 QY 481 ACAGATGAATTCGACAGAACTCAGCGGTAAAGCGGTATCCACCGCTTAGGTATGAC 540  
 DB 481 ACAGATGAATTCGACAGAACTCAGCGGTAAAGCGGTATCCACCGCTTAGGTATGAC 540  
 QY 541 GGTGTTGATATATTTCCGGAGAACGTCCTTCCCAATCTTTACCGAGTCCGGGAACGGTG 600  
 DB 541 GGTGTTGATATATTTCCGGAGAACGTCCTTCCCAATCTTTACCGAGTCCGGGAACGGTG 600  
 QY 601 GAATATCTGTTAACTGGCAATATATGACCGATGCAAAAGTATGATGAGAGGTGAGGG 660  
 DB 601 GAATATCTGTTAACTGGCAATATATGACCGATGCAAAAGTATGATGAGAGGTGAGGG 660  
 QY 661 GTTGCAATGCAATTTGGTATATACATTTATGTTATGTTATGTTATGTTATGTTATGTT 720  
 DB 661 GTTGCAATGCAATTTGGTATATACATTTATGTTATGTTATGTTATGTTATGTTATGTT 720  
 QY 721 TATGCGGTAAAGATGTGCAAGAAAGGAAAGAGCATCTGTCGCAAAATATACGTTGATTT 780  
 DB 721 TATGCGGTAAAGATGTGCAAGAAAGGAAAGAGCATCTGTCGCAAAATATACGTTGATTT 780  
 QY 781 GATAACAAACCATGAATGGCAAGCTGATTAATAATCAGTATGTCGCAAAATATAAAGAT 840  
 DB 781 GATAACAAACCATGAATGGCAAGCTGATTAATAATCAGTATGTCGCAAAATATAAAGAT 840  
 QY 841 GAACCCAAACACCGTACCATTTACGACATTTAGCAAAATTTGACGCGCAACCGCTTT 900  
 DB 841 GAACCCAAACACCGTACCATTTACGACATTTAGCAAAATTTGACGCGCAACCGCTTT 900  
 QY 901 ACCGGCAGTGCACAGTCAATCTGATTTAGCGAAAAACCTTGCGGTAATGAGCGTTTG 960  
 DB 901 ACCGGCAGTGCACAGTCAATCTGATTTAGCGAAAAACCTTGCGGTAATGAGCGTTTG 960

DB 901 ACCGGCAGTGCACAGTCAATCTGATTTAGCGAAAAACCTTGCGGTAATGAGCGTTTG 960  
 QY 961 TTTTTCATCCGATGCGGATCAGCGCTTGAAGGCGGTTTTCGCGGTAACGAGAA 1020  
 DB 961 TTTTTCATCCGATGCGGATCAGCGCTTGAAGGCGGTTTTCGCGGTAACGAGAA 1020  
 QY 1021 GAGCTTCCGAGCGGTTTATCAGCAACGACAAACAGCGTATTTCCGCGTATTCGAGGCAAA 1080  
 DB 1021 GAGCTTCCGAGCGGTTTATCAGCAACGACAAACAGCGTATTTCCGCGTATTCGAGGCAAA 1080  
 QY 1081 AAAACAGAGACAGCAACGACAGATACAAAACCTGCGCTGCGTCTGGAACACACACC 1140  
 DB 1081 AAAACAGAGACAGCAACGACAGATACAAAACCTGCGCTGCGTCTGGAACACACACC 1140  
 QY 1141 AAAATCTTGATTTCTTAAAAATTCGTTGACGAGGCGATGATGCGCATGCCCGTAAG 1200  
 DB 1141 AAAATCTTGATTTCTTAAAAATTCGTTGACGAGGCGATGATGCGCATGCCCGTAAG 1200  
 QY 1201 TTTGCCATTTCTCTATGCGCGATTTTGGTTCATCCGACAAATCTTGTGCGAAGGCGT 1260  
 DB 1201 TTTGCCATTTCTCTATGCGCGATTTTGGTTCATCCGACAAATCTTGTGCGAAGGCGT 1260  
 QY 1261 GAAATCTCTTTGTAACGAAAGAAATAATCAAGCTTGCAGCGGAGGAAATGACC 1320  
 DB 1261 GAAATCTCTTTGTAACGAAAGAAATAATCAAGCTTGCAGCGGAGGAAATGACC 1320  
 QY 1321 GTCCGCTCTGTCGACTTTTTCGACTATGCTGAAACTCGGACGATAAACCGATCGC 1380  
 DB 1321 GTCCGCTCTGTCGACTTTTTCGACTATGCTGAAACTCGGACGATAAACCGATCGC 1380  
 QY 1381 CCGCAAGTAAACCAAGGCGGAAAGATAAGGGGAGGATGAAGGGTTCGAGGCTTCAT 1440  
 DB 1381 CCGCAAGTAAACCAAGGCGGAAAGATAAGGGGAGGATGAAGGGTTCGAGGCTTCAT 1440  
 QY 1441 AACCAAGAAAGAAAGCGAAGCGGCTAGAGCGGCGGGAAGAGAGAGAACT 1500  
 DB 1441 AACCAAGAAAGAAAGCGAAGCGGCTAGAGCGGCGGGAAGAGAGAGAACT 1500  
 QY 1501 TCCGAGAGGATATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
 DB 1501 TCCGAGAGGATATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
 QY 1561 GATGAAGCGGAG 1620  
 DB 1561 GATGAAGCGGAG 1620  
 QY 1621 GCGGTTTCCAGGAG 1680  
 DB 1621 GCGGTTTCCAGGAG 1680  
 QY 1681 TTTCTGAAGAGTATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740  
 DB 1681 TTTCTGAAGAGTATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740  
 QY 1741 ACCGCACTTGGGAAGCGGATCGGCAAAACCCATTCAATGGGCAATCAGCGGATGAA 1800  
 DB 1741 ACCGCACTTGGGAAGCGGATCGGCAAAACCCATTCAATGGGCAATCAGCGGATGAA 1800  
 QY 1801 AAAGCGCAAAAG 1860  
 DB 1801 AAAGCGCAAAAG 1860  
 QY 1861 ACGAG 1920  
 DB 1861 ACGAG 1920  
 QY 1921 GGTTCCTCAGGAG 1980  
 DB 1921 GGTTCCTCAGGAG 1980  
 QY 1981 ACCGACCCCAAAACATTTCCAGCTAGTATCTTCTGTTAGAGAGAGAGAGAGAG 2040  
 DB 1981 ACCGACCCCAAAACATTTCCAGCTAGTATCTTCTGTTAGAGAGAGAGAGAGAG 2040



Db	62677	CCGACAGAAGAGCGGCGGTTTCAGACGGCATCTCCCGCTCCGGAAGCCCTTAA	62618
Qy	1663	GGCAGGACATCGACCTTTCTGAAAGGTATCCGACGCGCAGAAACGGATATTCGCGAA	1722
Db	62617	GGCAGGACATCGACCTTTCTGAAAGGTATCCGACGCGGGAACGGATATTCGCGAA	62558
Qy	1723	AGCGGAACGGCGCATTTACCGGACATTTGGGAAGCGGTATCGGCAACCCATTCATGG	1782
Db	62557	ACTGGAGAAGCACACTATACCGGACCTTGGGAAGCGGTATCGGCAACCCATTCATGG	62498
Qy	1783	GACATCAGCGGGTGAAGAGCGGCAAGAGCAGAAATTTACGTTGATTTGCACAAGAAA	1842
Db	62497	GACATCAGCGGGTGAAGAGCGGCAAGAGCAGAAATTTACGTTGATTTGCACAAGAAA	62438
Qy	1843	TCGATTTCCGGAAGCTGACGAGCAAAACCGCGTAGAACCTGCTTTCCATATTTGAAGAC	1902
Db	62437	TCGATTTCCGGAAGCTGACGAGCAAAACCGCGTAGAACCTGCTTTCCATATTTGAAGAC	62378
Qy	1903	GGCAAGATGATGGCAACGGTTTCCAGCGACGCGGACCTCGGGAGAGCGGCATCAAT	1962
Db	62377	GGCAAGATGATGGCAACGGTTTCTACCGACAGCACGCGCTCGGGAGAGCGGCATCAAT	62318
Qy	1963	CTTTCCGGAAGTGTTCGACCGACCCCAAAACATTCGAAGCTAGTAATCTTCGTGTAGAA	2022
Db	62317	CTTTCCGGAAGTGTTCGACCGACCCCAAAACATTCGAAGCTAGTAATCTTCGTGTAGAA	62258
Qy	2023	GGAGGATTTAGCGCCCGCGGCGGAATTTGGCGGTACTTATTTCAATATGATGG	2082
Db	62257	GGGGGATTTAGCGCCCGCGGCGGAATTTGGCGGTACTTATTTCAATATGATGG	62198
Qy	2083	AAATCTCTAGTATTAACGAAATATTTGAAATGAACTGAAGCTGAAGTTCGAAGTGA	2142
Db	62197	AAATCTCTAGTATTAACGAAATATTTGAAATGAACTGAAGTTCGAAGTTCGAAGTGA	62156
Qy	2143	GCTGAAGCTGAAGTTGAACTGCAAGCTGATTTGGCAACAGTTAGAACCTGATGAAGTT	2202
Db	62155	GTTGAAGCTGAAGTTGATGCTGAAGTTGATTTGGCAACAGTTAGATC---TGAAGTT	62099
Qy	2203	AAACACAAATTCGGCGTGTATTCGGTGGCAAGAAATATGATGAGAGGTGGAATAATGA	2262
Db	62098	AAACACAAATTCGGCGTGTATTCGGTGGCAAGAAATATGATGAGAGGTGGAATAATGA	62039
RESULT 3			
Id	AAF21611/c		
Xx	AAF21611 standard; DNA; 349980 BP.		
Ac	AAF21611;		
Xx	13-MAR-2001 (first entry)		
Dt	Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.		
Xx	Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;		
Xx	diagnosis; antigen; detection; infection; gene therapy; antibacterial;		
Xx	Qy.		
Os	Neisseria meningitidis.		
Xx	WO200066791-A1.		
Pn	09-NOV-2000.		
Pd	08-MAR-2000; 2000WO-US005928.		
Pf	30-APR-1999; 99US-0132068P.		
Pr	08-OCT-1999; 99WO-US023573.		
Pr	28-FEB-2000; 2000GB-00004695.		
Xx	(CHIR ) CHIRON CORP.		
Pa	(GENO-) INST GENOMIC RES.		
Xx			

PI	Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;	
PI	Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;	
PI	Rappuoli R, Frazer CM, Grandi G;	
XX	WPI; 2000-647603/62.	
XX	Neisseria meningitidis B full length genome sequence and open reading	
XX	frames are used to detect, treat and prevent Neisserial infections.	
PT	Claim 7; Appendix A; 692pp; English.	
PS	The present invention describes the full length genome of Neisseria	
CC	meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613	
CC	represent fragments of the NMB genomic sequence, as the sequence was too	
CC	long to go in a record on its own it was split into 8 sequences which	
CC	overlap each other at the beginning and end of each sequence by 49980 bp	
CC	(i.e. the last 49980 bp of AAF21544 is repeated at the beginning of	
CC	AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of	
CC	AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins	
CC	primers which are used in the exemplification of the present invention.	
CC	The NMB genome and fragments from it have antibacterial activity, and can	
CC	be used in vaccines and gene therapy. Neisseria nucleic acids, proteins	
CC	and/or antibodies which binds to the proteins can be used in compositions	
CC	for treating or preventing infection due to Neisserial bacteria or as a	
CC	diagnostic reagent for detecting the presence of Neisserial bacteria or	
CC	of antibodies raised to Neisserial bacteria. Computers, computer memory,	
CC	computer storage medium or computer databases can be used in a search to	
CC	identify open reading frames (ORFs) or coding sequences within the NMB	
CC	genome. The DNA sequences provide further opportunities to find antigenic	
CC	or immunogenic proteins which are more effective in vaccines than the	
CC	outer membrane proteins currently used	
XX	Sequence 349980 BP; 87189 A; 93501 C; 84627 G; 84663 T; 0 U; 0 Other;	
SQ	Query Match 68.9%; Score 1558; DB 3; Length 349980;	
	Best Local Similarity 83.6%; Pred. No. 0;	
	Matches 1906; Conservative 0; Mismatches 290; Indels 84; Gaps 9;	
Qy	1 ATGTGTAACCAATATGGCGCATTTGCTGTGTGCGCTTACTTTAGCATCTTGTATC 60	
Db	99481 ATGTGTAACCAATATGGCGCATTTGCTGTGTGCGCTTACTTTAGCATCTTGTATC 99422	
Qy	61 GGCGGCAATTCGGCGTACAGCTGTGTGCGAATCAACCGCGACCGCGCAACTCTGTCA 120	
Db	99421 GGCGGCAATTCGGCGTACAGCTGTGTGCGAATCAACCGCGACCGCGCAACTCTGTCA 99374	
Qy	121 GATTCGCAATCTTCCAAATCTAAGGACGTTCCCACTCCCGCCCTCTCCGGTATTCGGTA 180	
Db	99373 TACCCCGTCACTTCAAAATCTAAGGACGTTCCCACTCCCGCCCTCTCCGGTATTCGGTA 99314	
Qy	181 GAATTCACCGCGTCAAGCGCCCGCGTGGGCAATCGCGCTGCGGCAATCGGCGCGAAT 240	
Db	99313 GAATTCACCGCGTCAAGCGCCCGCGTGGGCAATCGCGCTGCGGCAATCGGCGCGAAT 99254	
Qy	241 ATCGCAATCTTTGATAAAAAATGTAATGTAATTTCCCAATAGTAAGCAGGAGGATAT 300	
Db	99253 ATGCTTCTCTATAAACAAGACGCGTACGGAATTTCCGCAAGCATCAGGAGGAGCAT 99194	
Qy	301 CTGCGCTCAAGAGAGGATATCTGTTTTTAGAGGTCACCGCAAGCAAGACGAGCTGAC 360	
Db	99193 CTGCGCTTAAAGAGAGGATATCTGTTTTTAGAGGTCACCGCAAGCAAGACGAGCTGAC 99134	
Qy	361 AAACCTTAAAGAGGAAATCAACGACGGCATCTTAATGCAACCAATCTACAGCTCCGATTTA 420	
Db	99133 AAACCTTAAAGAGGAAATCAACGACGGCATCTTAATGCAACCAATCTACAGCTCCGATTTA 99074	
Qy	421 AAAGATGATCGGTATCAATATAATATGTCGGGCGGATATGTTTATATAGATATGA 480	
Db	99073 GAAGAAGAAAAATATCAATATCAATTTGTCGGTGGGCTATGTTGTACAGGCGGAA 99014	
Qy	481 ACA-----GATGAATCGAAGCAAGTACGGGTAAGCGGTGTACCCACCGCTAGGT 534	



Db 99013 GGAAGGATAATGAAAAAGAAAGACTTCTGTAGTAAAGAGTTTCTTAACCGATTAGT 98954  
 QY 535 TATGACGGTTTGTATATATATCCGAGAGACGTCTTCCCAATCTTTTACCGAGTCGGGA 594  
 Db 98953 TATGACGGTTTGTATATATATCCGAGAGACGTCTTCCCAATCTTTTACCGAGTCGGGA 98894  
 QY 595 ACGGTGGAATATTTCTGTAACCTGGCAATATATGACCGATGCCAAAGCTCATCGACAGGT 654  
 Db 98893 ACGGTGCAATATTTCCGTAACTGGCAATATATGACCGATGCCAAAGCTCATCGACAGGT 98834  
 QY 655 CAGGCGGTTGGCAATGACAAATTTGGGTATATACATTTATGTTAAACGATGTTGGTGA 714  
 Db 98833 AAGCGGTTTTCAGTACGCAATTTGGGTATATACATTTATGTTAAATGGAATGCGGCA 98774  
 QY 715 ACTTCTTATGCGGTAAGGATGTCGACGAAAGGGAAGCAATCTTCCCAATATATACAGTT 774  
 Db 98773 ACTTCTTATGCGGTAAGGATGTCGACGAAAGGGAAGCAATCTTCCCAATATATACAGTT 98714  
 QY 775 GATTTTGATAACAAACCATGATGCAAGCTGATTAATAATCAGTATGTGCAATAAA 834  
 Db 98713 GATTTTGATAACAAACCATGATGCAAGCTGATTAATAATCAGTATGTGCAATAAA 98654  
 QY 835 A-----AAGATGAACCCAAAACCGCTGACCATTTACGACATTTACCGCAATTTGAC 888  
 Db 98653 AGTAATCCAAATGAGCCCAAAACCGCTGACCATTTACGACATTTACCGCAATTTGAC 98594  
 QY 889 GGCACCGCTTTACCGGAGTCGCAAGCTCAATCTGATTTAGCGAAACCTTCCCGGT 948  
 Db 98593 GGCACCGCTTTACCGGAGTCGCAAGCTCAATCTGATTTAGCGAAACCTTCCCGGT 948  
 QY 949 AATGAGCGTTTGTCTTCCATGCCATGCCATGATGAGCGGCTTGGCGGCTTTTTCGGC 1008  
 Db 98533 AAAGAATATTTGTTTCCATACCGATGCCATGAGCGGCTTGGCGGCTTTTTCGGC 98474  
 QY 1009 GATACGAGAGAGCTTGGCGGAGCTTTATACGACAAACAGAGCTATTCGGCGTA 1068  
 Db 98473 GATACGAGAGAGCTTGGCGGAGCTTTATACGACAAACAGAGCTATTCGGCGTA 98414  
 QY 1069 TTCCGAGCA---AAACAGAGACACCAACCGAGAGATACAAACCTTCCCGTCCG 1125  
 Db 98413 TTCCGAGCAACCAACAGAGACACCAACCGAGAGATACAAACCTTCCCGTCCG 98354  
 QY 1126 TCTGGAACACACCAACCTTCTGATTTCTTAAATAATTCGTTGAGCGGCACTGAT 1185  
 Db 98353 TCTGGAACACACCAACCTTCTGATTTCTTAAATAATTCGTTGAGCGGCACTGAT 98294  
 QY 1186 GGCCATGCCGTAAAGTTTGCATTTCTTATGCCGATTTTGTGTCATCCCGCAAACTT 1245  
 Db 98293 AAAAATCCCGTGAGTTTGGCAATTTCTCTATGCCGATTTTGTGTCATCCCGCAAACTT 98234  
 QY 1246 CTGTGCAAGGGCTGAAATTCCTTGTGTAACGAGAAACAAATCATCAAGCTTGGCGAC 1305  
 Db 98233 CTGTGCAAGGGCTGAAATTCCTTGTGTAACGAGAAACAAATCATCAAGCTTGGCGAC 98174  
 QY 1306 GGCAAGAAATGACCGTCCGTGCTTGTGCGACTTTTGTGCTATGTAACCTCGGACGG 1365  
 Db 98173 GGTAGGAAACGCAATCCGAACTCTGCTGATTTCTGACCTATGTAACCTCGGACGG 98114  
 QY 1366 ATAAACCGATGCCCGGCAAGTAACCAAGCGGAAAGATAAAGGGGAGGATGAAGAG 1425  
 Db 98113 ATGCAACCGAAGCTCCCGCGCAACCGAAGCGGAGGAGGAGGAGGAGGAG 98054  
 QY 1426 GGTGCGGCTTGTATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1485  
 Db 98053 GATACGCGGTTGATGCGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 97994  
 QY 1486 GAAGAAGACCAAACTTCCGAGAGGATATATGCGGAGGAGGAGGAGGAGGAGGAGGAG 1545  
 Db 97993 GAAGAG-----CAGCGGTAAACGAGGAGGAGGAGGAGGAGGAGGAGGAG 97955  
 QY 1546 GAAACGAGAGGTTGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1605  
 Db 97954 GAAGCGGTGAAGGT-----GAAGATGAGCTGAAGAACCCGAGAGGAGGAGGAGGAG 97907

QY 1606 CCG---GCAGAGAGCAACGGCGGTTTCAGGAGCATCTCCCTGCTAGAGCTCTAAA 1662  
 Db 97906 CCGAGAGAGAGGCGGAGCGGTTTCAGAGCGCATCTCCGCTCCGAGAGCCCTAAA 97847  
 QY 1663 GGCAGGACATCGACCTTTTCTGTAAGAGTATCCGACCGGAGAAACGGATATTCGCAA 1722  
 Db 97846 GGCAGGACATCGACCTTTTCTGTAAGAGTATCCGACCGGAGAAACGGATATTCGCAA 97787  
 QY 1723 AGCGGAACGGCGCATTTATACGCGACTTGGGAAGCGGCTATCGGCAACCCATTCATGG 1782  
 Db 97786 ACTGGAAGACACTATACCGGCACTTGGGAAGCGGCTATCGGCAACCCATTCATGG 97727  
 QY 1783 GACAACTCAGGCGGATGAAAGCGGCAAAAGCAGAAATTTACCGTTGATTTCCGACAGAA 1842  
 Db 97726 GACAACTCAGGCGGATGAAAGCGGCAAAAGCAGAAATTTACCGTTGATTTCCGACAGAA 97667  
 QY 1843 TCGATTTCCGGAAGCTGACGAGCAAAACCGCGTAGAACCTGCTTTCCATATTGAAGAC 1902  
 Db 97666 TCGATTTCCGGAAGCTGACGAGCAAAACCGCGTAGAACCTGCTTTCCATATTGAAGAC 97607  
 QY 1903 GGCAGATGATGCAACGCTTCCACGCGACCGCGCATCTCGGAGAGCGGCATCAAT 1962  
 Db 97606 GGCAGATGATGCAACGCTTCCACGCGACCGCGCATCTCGGAGAGCGGCATCAAT 97547  
 QY 1963 CTTTCCGGAATGTTTCGACCGACCCCAAAACATTTCCAAAGCTAGTAATCTTCGTGTAGAA 2022  
 Db 97546 CTTTCCGGAATGTTTCGACCGACCCCAAAACATTTCCAAAGCTAGTAATCTTCGTGTAGAA 97487  
 QY 2023 GGAGATTTTACGCGCGCGAGCGCGGATTTGGCGGTACTATTTTCAATAATGATCGG 2082  
 Db 97486 GGGGATTTTACGCGCGCGAGGATTTGGCGGTACTATTTTCAATAATGATCGG 97427  
 QY 2083 AAATCTCTTACTATACTGAAATATTTGAAATGAACTGAACTGAACTGAACTGAA 2142  
 Db 97426 AAATCTCTTACTATACTGAAATATTTGAAATGAACTGAACTGAACTGAA 97385  
 QY 2143 GCTGAAGCTGAAGTTGAAGTTGAAGCTGATCTGGCAACAGTTAGAACCTGATGAGTT 2202  
 Db 97384 GTTGAAGCTGAAGTTGAAGTTGAAGCTGATCTGGCAACAGTTAGAACCTGATGAGTT 97328  
 QY 2203 AAACACAAATTCGCGGTGTTATTCGTCGCAAGAAAGATATSCAGAGGAGTGGAAAAATGA 2262  
 Db 97327 AAACACAAATTCGCGGTGTTATTCGTCGCAAGAAAGATATSCAGAGGAGTGGAAAAATGA 97268

RESULT 4

AAX23319  
 ID AAX23319 standard; cDNA; 2277 BP.  
 XX AAX23319;  
 AC AC  
 XX XX  
 DT 11-JUN-1999 (first entry)  
 XX

N. meningitidis strain BNCV LbpB cDNA.

lbpB; lactoferrin binding protein; vaccine; neisserial disease; meningitis; diagnosis; treatment; ds.

Neisseria meningitidis.

Key Location/Qualifiers  
 CDS 100..2277  
 FT /\*tag= a  
 FT /product= "LbpB"  
 XX

MO9909176-AL.

XX

XX

XX

XX

XX

XX





Dd	409	GAATAATATAAATATGTTATGAAATTTGTAGATCGAGTTATGATATACATAAAGGGA	468
Qy	481	ACAGATGAAATCGAACAACTCAGGCGGTAAAGCGGTTACCCACCGCTTAGGTTATGAC	540
Dd	469	AAAGATGAAATTTGAGTGACTTCAAAATCACAGCAGTTTACTACCGGTTTGGTTATGAC	528
Qy	541	GGTTTTGTATATTTACCGGAGACGTCCTTCCAACTTTTACCGAGTCCGCGAACGCTG	600
Dd	529	GGTTTTGTATATTTACCGGAGACATCTTTCCAACTTTTACCGAGCGCGGAAACGCTG	588
Qy	601	GAATATCTGTGTAATCTGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTCAGGC	659
Dd	589	AAATATCTCGGCACTGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTAAGCA	648
Qy	660	--GGTTGGCATTGACAAATTTGGGTTATATCAATTTTATGTAACGATTTGGTGCAACT	717
Dd	649	GGAGATCTTAGCGAAGATTTGGGTTATATCGTTTATTACGGTCAAAATGTTCGGAGCACT	708
Qy	718	TCTATGCGGCTTAAGATGTGACGAGGGAAGAGCATCTGCCAAATATACGCTTGAT	777
Dd	709	TCTTATGCTGCACTGCGGACGACCGAGAGGGAACATCTCGCGAATATACGCTAGAT	768
Qy	778	TTTGATAACAAACCATGAATGGCAAGCTGATTAATAAATCAGTATGTGCAAAATAAAAA	837
Dd	769	TTTCGGTAAGAAACTTTGACGGTAAATTAATTAATAATCAGTATGTGCAAAAGAAACC	828
Qy	838	GATGAACCCAAAAACCGCTGACCAATTTACGATTAACGATTAACGATTAACGATTAACG	897
Dd	829	GATGAA--AAGAAACCGCTGACCAATTTACGACATTTACTGCAACATTTGACGCGCAACCGC	885
Qy	898	TTTACCGGAGTGCAGAGTCAATCTGATTTAGCGMAAAACCTTGCGGTAATGAGCGT	957
Dd	886	TTTACCGGAGTGCAGAGTCAATCTGATTTAGCGMAAAACCTTGCGGTAATGAGCGT	945
Qy	958	TTGTTTTTCCATGCGGATCCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCGATTAACGGA	1017
Dd	946	TTGTTTTTCCATCAGATCCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCGATTAACGGA	1005
Qy	1018	GAAAGCTTTCGGGACGTTTATCAGCAACGACAGCGATTTGCGCGATTTTCGCGGCTTTCG	1077
Dd	1006	GAAAGCTTTCGGGACGTTTATCAGCAACGACAGCGATTTGCGCGATTTTCGCGGCTTTCG	1065
Qy	1078	A--AAACACAGACAGCAACGACAGCAGATACAAACCTGCGGCTGCTCGAAAAA	1134
Dd	1066	AAACAAAAACAGACGCACTCAAGCATCAGATCAAACTCTGCTATGCGCTCTGAATAA	1125
Qy	1135	CACACAAAAATCTTGATTTCTTAAATAATTTCCGTTGACGAGCGGCTGATGCGCATGCC	1194
Dd	1126	CACACAAAAATCTTGATTTCTTAAATAATTTCCGTTGACGAGCGGCTGATGCAATGCC	1185
Qy	1195	CGTAAGTTTGCATTTCTTATGCGCGATTTTGGTCATCTCCGACAAACTTCTTGTGAA	1254
Dd	1186	CGTAAGTTTGCATTTCTTATGCGCGATTTTGGTCATCTCCGACAAACTTCTTGTGAA	1245
Qy	1255	GGCGGTGAATCTCTTTGTTAAACAGAAACAATCATCAAGCTTCCGACGCGCAGGAA	1314
Dd	1246	GGCGGTGAATCTCTTTGTTCAAGATCTCAAACTCATCAAACTTTCGCGACGCGAGAA	1305
Qy	1315	ATGACCGTCCGTCGTTGTTGCGACTTTTGAACCTATGTGAACCTCGGACGGAATAAAC	1374
Dd	1306	ATGACCGTCACTGTTGTCGACTTTTTCGACCTATGTGAACCTCGGACGGAATAAAC	1365
Qy	1375	GATCGCGCGCAAGTAAACAAAGGCGGGAAGA-----TAAA	1410
Dd	1366	GACCGCGCGCAAGTAAACAAAGGCGGGAAGATGAAATTTCCGAGATGAAATTTGGTGAA	1425
Qy	1411	GGGAGAGATGAAGAGGTGCAGGCTTGTATAACGACGAAAGGCGGAAAGCAAGCGGTA	1470
Dd	1426	AGCGAGGAAATGAGAGGATTTGGTCGCTGAAGAGAAACACGAGAGCAAGTCTGTA	1485
Qy	1471	GAGACGAAGCGCGCAAGAGACGAACCTTCCGAGAGATTAATGCGGAGACGAAGAA	1530
Dd	1486	GAGATGAAGACAGAGAGAGAGACGAAGTTTCCGAGATGTTACAGTGAAGACGAAGAA	1545

Qy	1531	GCAACCGCGAAGAAAGAAACCGAAGAAAGTTGATGAAGCCGAAGAGGAGAAAGTTGAAGAA	1590
Dd	1546	GAATCTCCCGNA-----GAAGATGATGATGAGCCGAAGAGGAGAAAGTTGAAGAA	1596
Qy	1591	CCCGAAGAAATAATCCGCGGAGAAAGGCAAC---GGCGGTTCAGGACGATCTCTGCTGCC	1647
Dd	1597	CCCGAAGAAATAATCCGCGAAGAGCGCGGTTGCGGTTTCAGACGCGCATCCGCGCCCT	1656
Qy	1648	CTAGAAGCTCTAAGGCGAGGACATCGACCTTTTCTGAAAGGTATCCGCACGGCAAGAA	1707
Dd	1657	TCGGAAGCCCTTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATCCGCACGGCGAA	1716
Qy	1708	ACGATATTTCCGCAAGGCGGACCGCATTTATACCGGCACTTGGGAAGCGGTATCGGC	1767
Dd	1717	GCCGACATTCGCAAACTGGAAGACGCTATACCGGCACTTGGGAAGCGGTATCAGC	1776
Qy	1768	AAACCCATTCATGGAACAATCAGCGGATGAAAGCGGCAAGACGAATTTACCGTT	1827
Dd	1777	AAACCCATTCATGGAATAAAGCGGATTAAGAAAGCGCAAAAGCAGAAATTTGACGTT	1836
Qy	1828	GATTTTCGACAAAGATCGATTTTCGGAAGCTGACGAGACAAACCGGCTAGAACTGCT	1887
Dd	1837	GATTTTCGCGAAGAAATCGATTTTCGGAAGCTGACGAGAAACCGGTAGAGCTGCT	1896
Qy	1888	TTCCATATTTGAAGACGCGCAAGATTTGATGGCAACGGTTTCCACGCAACGCGGCACTCG	1947
Dd	1897	TTCTATATTTGAAGAGGTGATTTGATGGCAACGGTTTCCACGCAACGCGGCACTCG	1956
Qy	1948	GAGACGCGCATCAATCTTTTCGGGAAATGGTTGACCGGACCCCAAAACATTTCCAGCTAGT	2007
Dd	1957	GATACGCGCATCAATCTTTTCGGGAAATGGTTGACCAACCCCAAAACCTTCCAGCTAGT	2016
Qy	2008	ATCTTTCGTTAGAGGAGGATTTTACGCGCCGCGAGCGCGCAATTTGGGCGGTACTATT	2067
Dd	2017	GATCTTCGTTAGAGGAGGATTTTACGCGCCGCGAGCGGAGATTTGGGCGGTACTATT	2076
Qy	2068	TTCAATATATGATGGGAAATCTCTTAGTATACTGAAATAATTTGAAATAATGAAGCTGAA	2127
Dd	2077	TTCAATATGATGGGAAATCTCTTAGTATACTGAAATAATTTGAAATAATTTGAAATAAT	2123
Qy	2128	GAAATTTGAAGTTGAAGCTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAG	2187
Dd	2124	-----TGAAATTTGAAGCTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAG	2154
Qy	2188	GAACTGTAGAGTTAAACACAAATTTCCGCGTGGTATTCCGTCGCAAGAAAGATATGCAG	2247
Dd	2155	GAACT---TGAAATTTAAACCCCAATTTCCGCGTGGTATTCCGTCGCAAGAAAGATATGCAG	2211
Qy	2248	GAGGTGGAATAATGA	2262
Dd	2212	GAGGTGGAATAATGA	2226

RESULT 6  
AAAX23321  
ID AAX23321 standard; cDNA; 2226 BP.  
XX AAX23321;  
AC AAX23321;  
XX  
DT 11-JUN-1999 (first entry)  
XX  
XX N. meningitidis strain H44/76 LbpB cDNA.  
DE  
XX  
XX LbpB; lactoferrin binding protein; vaccine; neisserial disease;  
KW meningitis; diagnosis; treatment; ds.  
XX  
XX Neisseria meningitidis.  
OS  
XX  
XX Location/Qualifiers  
PH 1..2226  
FT /\*tag= a  
FT /product= "LbpB"

XX WO9909176-A1.  
 XX 25-FEB-1999.  
 XX 10-AUG-1998; 98WO-EP005117.  
 XX 15-AUG-1997; 97GB-00017423.  
 XX 05-FEB-1998; 98GB-00002544.  
 XX (UYUT-) RIJKSUNIV UTRECHT.  
 XX (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.  
 XX Pettersson-Fernholm AM, Tommassen JPM;  
 XX WPI; 1999-190165/16.  
 XX P-PSDB; AAW93494.  
 XX New lactoferrin-binding protein B polynucleotides - obtained from  
 PT Neisseria meningitidis, used to develop products for the diagnosis,  
 PT prevention and treatment of neisserial disease, e.g. meningitis.  
 XX Claim 2; Page 90-94; 116pp; English.  
 XX This invention describes novel lactoferrin-binding protein B (LbpB)  
 CC strains of Neisseria meningitidis. The products of this invention can be  
 CC used for vaccinating humans against neisserial disease e.g. meningitis.  
 CC Antibodies raised against the proteins of the invention can be used for  
 CC diagnosing or treating neisserial disease in humans. The LbpB  
 CC polypeptides can also be used for identifying compounds which inhibit the  
 CC polypeptides  
 XX Sequence 2226 BP; 683 A; 483 C; 571 G; 489 T; 0 U; 0 Other;  
 SQ  
 Query Match 63.8%; Score 1442.2; DB 2; Length 2226;  
 Best Local Similarity 80.3%; Pred. No. 0;  
 Matches 1828; Conservative 0; Mismatches 383; Indels 56; Gaps 9;  
 QY 1 ATGTGTAACCGAATTATGGCGGCAATGCTGTGTCCTTACCTTTAGCAATCTGTATC 60  
 DB 1 ATGTGTAACCGAATTATGGCGGCAATGCTGTGTCCTTACCTTTAGCAATCTGTATC 60  
 QY 61 GCGCGCAATTCGCGGTACAGCTGTGTCGAATCAACGCGCGCGCGCGCGCGCGCG 120  
 DB 61 GCGCGCAATTCGCGGTACAGCTGTGTCGAATCAACGCGCGCGCGCGCGCGCGCG 108  
 QY 121 GATTCGCAATCTTCCAACTCTGCGGATAGGCTGTCTCCAGCTCTGCGCGCGCTTCGTA 180  
 DB 109 TACCCCGTCACTTCAAGTCTAAGGACGTTCCCACTCGCGCCCTGCGCAACCTTCTATA 168  
 QY 181 GAAATCAGCGGT-----CAAGCGCGCGCGCTCGGTGGGCAATGCGGCTGCCAAG 234  
 DB 169 GAAACCAAGCGCGGTGCGGTCAACGCGCGCTCGGTGGGCAATGCGGCTGTGAGG 228  
 QY 235 CGGAATATCGCAACTTTTGATAAAATGGTAATCAAAATTCGAATAGTAAAGCGCGAG 294  
 DB 229 CGGATTTTCGCACTTCTGATAGGTTGGCAATGATTTTCCAAATAGCAACAAGCGAA 288  
 QY 295 GAGTATCGCGCTCAAGAGAGAGATATCTGTTTATAGCGGTAGCGCGGAAAGACAG 354  
 DB 289 GAAAGCTGTGTTTAAAGAGGATGATGTTCTGTTTATATAGCTTCAAAAAGATATA 348  
 QY 355 GCTGACAACTTAAAGAGGAATCAAGGCGGATCTTATGACCAATCTACAGTCC 414  
 DB 349 CTTCAGTGGCTTAAAGGATAAAATTCATCAACGCAATCTTATGTAGAAATTAGGACATCA 408  
 QY 415 GATTTAAAGATGATGATCAATATAAATATCTCGGCGCGATATGTTTATCTAGA 474  
 DB 409 GAAATGAATAAATAATATGTTATGAAATTTGTGGATGCGGTTATGTATATACTAAA 468  
 QY 475 TATGGAACAGATGAAATCGAACAGAACTCAGGCGGTAAAGCGGTTTACCCCGCTTAGGT 534  
 DB 469 AACGGAACAGATGAAATGAGTGGACTTCAAAATCGCAAGCAATTTCTTAATCGTTTGGC 528

QY 535 TATGACGGTTTGTATATTAATTCGAGAGAACTGCTTCCCAATCTTTACCGAGTCGGGA 594  
 DB TACGACGGTTTGTATATTAATTCGAGAGAACTGCTTCCCAATCTTTACCGAGTCGGGA 588  
 QY 595 ACGGTGGAATATCTGGTAACTGGCAATATATGACCGATGCCAAACGTCATCGACAGGT 654  
 DB ACGGTGCAATATTCGGTAACTGGCAATATATGACCGATGCCAAACGTCATCGACAGGT 648  
 QY 655 CAGGC---GGTTGGCATTGACAAATTTGGTGTATATACATTTTATGTTAAACGATGTTGT 711  
 DB AAAGCAGAGATCTTACGAGATTTGGTGTATCTCGTTTATACGTTAAATGTCGGA 708  
 QY 712 GCAACTTCTTATGCGCTAAGATGTCGACGAAAGGAAAGCATCTCTGCCAAATATACG 771  
 DB GCAACTTCTTATGCTGCGACTGCCGACGACGCGGAGGAGGAAACATCTCTGCCAAATATACG 768  
 QY 772 GTTGATTTTGTATACAAACCATGATGATGCGAAGCTGATTAATAATCAGTATGTGGAAT 831  
 DB GTTGATTTTGTATACAAACCATGATGATGCGAAGCTGATTAATAATCAGTATGTGGAAT 828  
 QY 832 AAAAAAGATGAACCCCAAAAAACCGCTGACCATTTTACGACATTTACTGCAAAATTTGACCGC 891  
 DB AAAAAAGATGAACCCCAAAAAACCGCTGACCATTTTACGACATTTACTGCAAAATTTGACCGC 885  
 QY 892 AACCGCTTTACCGGAGTCGCAAGTCAATCTGATTTAGCGGAAACCTTTGCCGCTATC 951  
 DB AACCGCTTTACCGGAGTCGCAAGTCAATCTGATTTAGCGGAAACCTTTGCCGCTATC 945  
 QY 952 GAGCGTTTGTGTTTCCATGCGGATGCGATCAGCGGCTTGAAGGCGGTTTTCGCGCAT 1011  
 DB GAGCATTTGTTTTCATACCGATGCGGATCAGCGGCTTGAAGGCGGTTTTCGCGCAT 1005  
 QY 1012 AACCGAGAGAGCTTTGCCGAGCTTTTATCAGCAACGACACACAGCTATTCGGCGTATTC 1071  
 DB AAGCGGAGAGCTTTGCCGAGCTTTTATCAGCAACGACACACAGCTATTCGGCGTATTC 1065  
 QY 1072 GCAGGCAAAAAACAGAGACAGCAAAACGACAGATACAAACCTGCGCTCTGGA 1131  
 DB GCAGGCAAAAAACAGAGACAGCAAAACGACAGATACAAACCTGCGCTCTGGA 1125  
 QY 1132 AAACACACCAAAATCTTGGATCTCTAAATTTTCGTTGACGAGGCGACTGATGGCAT 1191  
 DB AAACACACCAAAATCTTGGATCTCTAAATTTTCGTTGACGAGGCGACTGATGGCAT 1185  
 QY 1192 GCGCGTAAGTTTGCACTTCTCTATGCCGATTTTGTCTCATCCCGACAAACTCTTTGTC 1251  
 DB GCGCGCGGTTTGCACTTCTCTATGCCGATTTTGTCTCATCCCGACAAACTCTTTGTC 1245  
 QY 1252 GAAGGCGTGAAATTCCTTTGGTAAACGAGAAACAAATCATCAAGCTTTGCCGAGCGAGG 1311  
 DB GAAGGCGTGAAATTCCTTTGGTAAACGAGAAACAAATCATCAAGCTTTGCCGAGCGAGG 1305  
 QY 1312 AAATGACCGTCCGTGCTTGTGCGACTTTTGTGACCTTATGTGAACTCTCGGACGATAAA 1371  
 DB AAATGACCGTCCGTGCTTGTGCGACTTTTGTGACCTTATGTGAACTCTCGGACGATAAA 1365  
 QY 1372 ACCGATCGCGCGCAAGTAAACCAAGCGGAGATAAAGGAGGAGATGAGAGGTCGA 1431  
 DB ACTGACCGCGCGCAAGTAAACCAAGCGGAGATAAAGGAGGAGATGAGAGGATACA 1425  
 QY 1432 GCGGTTGATTAACGACGAGAAAGC---GAAGACGAGCGCTAGAAAGCAGAGCGCGGAA 1488  
 DB GCGGTTGATTAACGACGAGAAAGC---GAAGACGAGCGCTAGAAAGCAGAGCGCGGAA 1485  
 QY 1489 GAAGACGAACTTCCGAAAGGATATATGGGAGAGAGAGAGAGAGAGAGAGAGAGAA 1548  
 DB GAAGACGAACTTCCGAAAGGATATATGGGAGAGAGAGAGAGAGAGAGAGAGAGAA 1536  
 QY 1549 ACCGAGAGAGCTTATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1608  
 DB AACGAGAGAGCTTATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1596

QY 1509 GCAGAGGACAC---GGGGTTCAGCGAGCATCTGCTGCTAGAGCCCTTAAGGC 1665  
 DB 1597 GCAGAGGCGCGGTGGTTCAGAGCGCATCTGCTGCTAGAGCCCTTAAGGC 1656  
 QY 1666 AGGACATCGACCTTTCTCTGAAAGGTATCCGCGAGCGAGAAAGGATATCCGCAAGC 1725  
 DB 1657 AGGATATCGACCTTTCTCTGAAAGGTATCCGCGAGCGAGAAAGGATATCCGCAAGC 1716  
 QY 1726 GGAACGGCGCATATACCGGCATTTGGGAGCGGTATCGGCAAAACCCATTCATATGGAC 1785  
 DB 1717 GGAAGACGACGATATACCGGCATTTGGGAGCGGTATCGGCAAAACCCATTCATATGGAC 1776  
 QY 1786 AATCAGGCGGATGAAGAGCGGCAAAAGCAGATTTACCGTTGATTTCCGCAAGAAATCG 1845  
 DB 1777 AATCATGCGGATAAAGAGCGGCAAAAGCAGATTTGACGTTGATTTCCGCGAGAAATCG 1836  
 QY 1846 ATTTCCGGAAGAGTACGAGCAAAACCGCGGTAGAACCTGCTTTCCATATTTGAAGACGC 1905  
 DB 1837 ATTTCCGGAAGAGTACGAGCAAAACCGCGGTAGAACCTGCTTTCCATATTTGAAGACGC 1896  
 QY 1906 AAGATGATGCAACGGTTTCCAGCGACGCGGCACTCGGAGAGCGGCATCATCTT 1965  
 DB 1897 GTGATTGAGGCAATGTTTCCAGCGACGCGGCACTCGGAGATACGCGCATCATCTT 1956  
 QY 1966 TCGGGAATGTTTCAGCGACCCCAAAACATTTCCAGCTAGTAATCTTCTGTTAGAGGA 2025  
 DB 1957 TCGGGAATGTTTCAGCTAATCTTCCAAAGTTTCAAGGCAATATCTTCTTGTACAGGC 2016  
 QY 2026 GGAATTTACGCGCGCGGAGGAAATTTGGGCGGTACTATTTTCAATAATGATGGAAA 2085  
 DB 2017 GGTATTTACGCGCGCGGAGGAAATTTGGGCGGTACTATTTTCAATAATGATGGAAA 2076  
 QY 2086 TCTCTAGTATAACGAAATATTTGAAATGAAGCTGAAGCTGAAGTTGAAGCT 2145  
 DB 2077 TCTCTAGTATAACGAAATATTTGAAATGAAGCTGAAGCTGAAGTTGAAGCT 2112  
 QY 2146 GAAGCTGAAGTTGAAGTTGAAGCTGATGTTGCAAAAGCTAGTGAAGCTTAA 2205  
 DB 2113 GAAGCTGAAGTTGAAGTTGAAGCTGATGTTGCAAAAGCTAGTGAAGCTTAA 2169  
 QY 2206 CACAAATTCGCGCGGTATTCGCGTGAAGAAAGATATGCGAGAGGTGGAATAATGA 2262  
 DB 2170 CCCCATTTCGCGGTATTCGCGTGAAGAAAGATATTAAGAGAGGTGGAATAATGA 2226

RESULT 7

AA23323  
 ID AAX23323 standard; cdNA; 2124 BP.

XX AAX23323;

XX AC AAX23323;

XX DT 11-JUN-1999 (first entry)

XX DE N. meningitidis strain 881607 LbpB cdNA.

XX KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;

XX KW meningitis; diagnosis; treatment; ds.

XX OS Neisseria meningitidis.

XX FH Key Location/Qualifiers

XX FT 1.-2124

XX FT \*tag= a

XX FT /product= "LbpB"

XX XX WO909176-A1.

XX PN 25-FEB-1999.

XX XX 10-AUG-1998; 98WO-EP005117.

XX XX 15-AUG-1997; 97GB-00017423.

XX PR 05-FEB-1998; 98GB-00002544.

XX SQ Sequence 2124 BP; 663 A; 461 C; 541 G; 459 T; 0 U; 0 Other;  
 Query Match 57.1%; Score 1291.8; DB 2; Length 2124;  
 Best Local Similarity 78.1%; Pred No. 1.6e-308;  
 Matches 1676; Conservative 0; Mismatches 417; Indels 54; Gaps 8;  
 QY 1 ATGTGTAACCGCAATTTATGCGGCATATGCTGTGTTGCTTACCTTTAGCATCTTGTATC 60  
 DB 1 ATGTGTAACCGCAATTTATGCGGCATATGCTGTGTTGCTTACCTTTAGCATCTTGTATC 60  
 QY 61 GCGGCAATTTGCGGTACAGCTGTTGTCGAATCAACGCGACGCGCAACTCTGCA 120  
 DB 61 GCGGCAATTTGCGGTACAGCTGTTGTCGAATCAACGCGACGCGCGG----- 108  
 QY 121 GATTCCCAATCTTCCAAATCTTCCGATAAGCTGCTCCAGCTCTCCGAGCCTTCGGTA 180  
 DB 109 TACCCCGTCACTTTCAAGCTTAAGACGTTCCACTTCGCTCTCCGGTCTTCGGTA 168  
 QY 181 GAAATCACCGCGTCAAGCGCGCGCGCTCGGTGCGCAATGCGGTGCGCAAGCGGAAT 240  
 DB 169 GAAACACCGCGGTCAACCGCGCGCGCTGCTGCGCAATGCGGTGCGCAAGCGGAAT 228  
 QY 241 ATCGCACTTTTGATAAAATGGAATGGAATTTCCCAATAGTAAGCAGCAGAGAT 300  
 DB 229 ATTGCACTTCTGATAAGATGGCAATGATTTTCCAAATAGCAAAACAGACAGAAAG 288  
 QY 301 CTGCGCTCAAGAGAGGATATCTGTTTATAGCGGTAGCGCGGTAGCGGAAAGAGAG 360  
 DB 289 CTGCTGTTAAGAGAGGATATCTGTTTATAGCGGTAGCGGAAAGAGAGAGAGAG 348  
 QY 361 AAATTTAAAGAGAAATCAAGCGGCGCATCTAATGACCAATCTACGTCGCAATTA 420  
 DB 349 CAGCTTAAAGATAAAATTCGTCAACCAATCTTACGCAAGCATTAACCATTCGGAAG 408  
 QY 421 AAAGATGATGCTATCAATATAAATATGTCGCGCGGATATGTTTATAGATATGGA 480  
 DB 409 AAAAAATAAAATATGATTAATAATTTGATGATGAGGTTATGATATATTAAGACGA 468  
 QY 481 ACAGATGAATCGAACAGAACTCAGCGGTAGCGGTTTACCACCGCTTAGGTATGAC 540  
 DB 469 AAAGATGAATTTGAGTGGACTTCAAAATTACAGAGCTCTACCAACCGGTTTGGTATGAC 528  
 QY 541 GGTGTTGATATATTTTCGAGAGAGCTGCTTCCCAATCTTTACCGAGTGGCGGAGCGTG 600  
 DB 529 GGTGTTGATATATTTTCGAGAGAGCTGCTTCCCAATCTTTACCGAGCGCGGAGCGTG 588  
 QY 601 GAATATCTGTAACCTGGCAATATATGACCGGATGCCAAACGTCATCGACAGCTCAGGC- 659  
 DB 589 AAATATTCGCAACTGCGCAATATATGACCGGATGCCATACGTCATCGACAGAGCA 648

(UYUT-) RIJKSUNIV UTRECHT.

(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.

Petersson-Fernholm AM, Tommassen JPM;

WPI; 1999-190165/16.

P-PSDB; AAW93496.

New lactoferrin-binding protein B polynucleotides - obtained from

Neisseria meningitidis, used to develop products for the diagnosis,

prevention and treatment of neisserial disease, e.g. meningitis.

Claim 2; Page 105-109; 116pp; English.

This invention describes novel lactoferrin-binding protein B (LbpB)

strains of Neisseria meningitidis. The products of this invention can be

used for vaccinating humans against neisserial disease e.g. meningitis.

Antibodies raised against the proteins of the invention can be used for

diagnosing or treating neisserial disease in humans. The LbpB

polypeptides can also be used for identifying compounds which inhibit the

polypeptides



QY 660 --GGTTGGCATTACAAATTTGGTTATATACACATTTTATGTAACGATCTTGGTCAACT 717  
 Db 649 GCGAGATCCTAGCGAGATTTGGTTATATCGTTTATTCGGTCAAAATGTGCGAGCAACT 708  
 QY 718 TCTTATGCGGCTAAGGATGTGCAAGAAAGGAAAGCATCTGCGCAAAATATACGGTTGAT 777  
 Db 709 TCTTATGCTGCACTGCCGACGACCGGAGGAGAAACATCTCTCCGCAATATACGGTTAT 768  
 QY 778 TTTGATAACAAACCAATGAATGGCAAGCTGATTAATAATCATGATGTGCGAAATAAAAA 837  
 Db 769 TTTGACACCAAAACCTCTGAATGGCAAGCTGATTAATAATCATGATGTGCGAAATAAAAA 825  
 QY 838 GATGAACCCAAAAACCGCTGACCATTTACGACATTTACGCAAAATTTGACGCGCAACCGC 897  
 Db 826 GATGATCTTAAAAACCACTGACCATTTACGCAAAATTTGACGCGCAACCGC 885  
 QY 898 TTTACCGGAGTCCCAAGTCAATCTGATTTAGCGAAAAACCTTGCCTGGTATGAGCGT 957  
 Db 886 TTTACCGGAGTCCCAAGTCAATCTGATTTAGCGAAAAACCTTGCCTGGTATGAGCGT 945  
 QY 958 TTTGTTTTCATGCGGATGCCGATCAGCGGCTTGAGGGCGGTTTTTTCGCGCATACCGGA 1017  
 Db 946 TTTGTTTTCATGCGGATGCCGATCAGCGGCTTGAGGGCGGTTTTTTCGCGCATACCGGG 1005  
 QY 1018 GAAAGAGCTTGCCTGACCGGTTTATCAGCAACGACACAGCGTATTCGCGGTATTCGACGC 1077  
 Db 1006 GAAAGAGCTTGCCTGACCGGTTTATCAGCAACGACACAGCGTATTCGCGGTATTCGACGC 1065  
 QY 1078 A---AAAAACAGACAGCAAAACGACGAGATACAAAACCTTGCCTGCTCGGAA 1134  
 Db 1066 AAACAAAAACAGACAGCAAAACGACGAGATACAAAACCTTGCCTGCTCGGAA 1125  
 QY 1135 CACACCAAAATCTGGATCTCTAAAAATTTCCGTTGACGAGCGACTGATGGCCATGCC 1194  
 Db 1126 CACACCAAAATCTGGATCTCTAAAAATTTCCGTTGACGAGCGAAAGTGGTGAATCCC 1185  
 QY 1195 CGTAAGTTGCAATTTCTCTATGCGCGATTTTGGTCAATCCGCAAACTTCTTGTGCA 1254  
 Db 1186 CGACGGTTGAGTTTCCATGATGCCCGATTTTGGTCAATCCGCAAACTTCTTGTGCA 1245  
 QY 1255 GGGCGTGAAATTCCTTTGGTAAACGAGAAACAAATCATCAAGCTTTCGCGAGCGAGGAA 1314  
 Db 1246 GGGCGTGAAATTCCTTTGGTAAACGAGAAACAAATCATCAAGCTTTCGCGAGCGAGGAA 1305  
 QY 1315 ATGACCGTCCGCTGTTGTCGATTTTGGTCAATCCGCAAACTTCTTGTGCA 1374  
 Db 1306 ATGACCGTCCGCTGTTGTCGATTTTGGTCAATCCGCAAACTTCTTGTGCA 1365  
 QY 1375 GATCGCCCGCAAGTAAACCAAGCGGAGATTAAGGGAGGATGAGAGGTTGCAAGC 1434  
 Db 1366 GATCGCCCGCAAGTAAACCAAGCGGAGATTAAGGGAGGATGAGAGGTTGCAAGC 1425  
 QY 1435 GTTGATAACGACGAGAAAGCGAGACGAGCCGTAGAGACGAGGCGCGAGAGAGAC 1494  
 Db 1426 GTTGATAACGAGTAAAGAAAGCGAGACGAGATCCGCGATGAGAGAGACGAGAGAG 1485  
 QY 1495 GAAACTTCCGAGAGGATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1554  
 Db 1486 G-----TCGTAGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1530  
 QY 1555 GAAGTTGATGAGCGGAG 1614  
 Db 1531 GAAGAGCTGAG 1590  
 QY 1615 GGCAACCGGCTTACGAGCATCTCTGCTGCTTACGAGGCTTAAAGGCGAGGACATC 1674  
 Db 1591 GGCAACCGGCTTACGAGCATCTCTGCTGCTTACGAGGCTTAAAGGCGAGGACATC 1650  
 QY 1675 GACCTTTCTGAAAGTATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1734  
 Db 1651 GACCTTTCTGAAAGTATCCGACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1710  
 QY 1735 CATTATACCGGCTTGGGAGCGCGTATCGGCAAC-----CCATTCAA 1779

Db 1711 CATTATACCGGCTTGGGAGCGGCTATCGGCTATCGGATAGTGGTACGTCCTCAAT 1770  
 QY 1780 TGGGCAATACGCGGATGAAAGCGGCAAAAGCAGAGATTTACCGTTGATTTGCAAG 1839  
 Db 1771 AAGGATAGCTATGCGGAAT---CAAGGGGCAAAAGCAGAGATTTACCGTTGATTTGCAAGCG 1827  
 QY 1840 AATCGATTTCCGGAAGCTGACGAGCAAAACCGGCTAGAACCTTCTTCCATATTGAA 1899  
 Db 1828 AAGACGCTTCCGGAATCTGACAGAAAAAATGATACACCCCGCTTTTATATTGAA 1887  
 QY 1900 GAGCGCAGATGATGCGCAAGGTTTCCACGCGCAGCGCACTCGGAGAGCGGCAATC 1959  
 Db 1898 AAGGTTGATGATGCGTAACGTTTCCACGCTTTGGCGCATCTCGGAGAGACGATTT 1947  
 QY 1960 AATCTTTCCGGAAGGTTTCCACGCGCAGCGCAATTTCCAGCTAGTAACTTCTGTTA 2019  
 Db 1948 GACCTTTCTGGCAGGTTTCCACGCGCAGCGCAATTTCAAAGCCGCAATCTTCTGTA 2007  
 QY 2020 GAAGGAGATTTTACGCGCGCAGCGCGGAGATTTGGCGGTACTATTTCATTAATGAT 2079  
 Db 2008 ACAGCGGCTTTTATGCGCGCGCAGCGCGCAGATTTGGCGGTATATTATTCAGACGAG 2067  
 QY 2080 GGGAAATCTCTAGTATTAATCTGAAATAATTTGAAATGAAGCTGAAGC 2126  
 Db 2068 CGGAAATTCGGTGGGTATTTGGGCGCAAAAGATGACAAAGGAGGC 2114

RESULT 8  
 AAX23320

ID AAX23320 standard; cDNA; 2169 BP.

AC AAX23320;

DT 11-JUN-1999 (first entry)

XX N. meningitidis strain M981 lbpB cDNA.

DE LbpB; lactoferrin binding protein; vaccine; neisserial disease;  
 KW meningitis; diagnosis; treatment; ds.

XX Neisseria meningitidis.

FH Key Location/Qualifiers  
 CDS 1..2169  
 FT /\*tag= a  
 FT /product= "lbpB"

XX WO9909176-A1.

XX 25-FEB-1999.

XX 10-AUG-1998; 98WO-EP005117.

XX 15-AUG-1997; 97GB-00017423.

XX 05-FEB-1998; 98GB-00002544.

XX (UYUT-) RIJKSUNIV UTRECHT.

PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.

XX Pettersson-Fernholm AM, Tommassen JPM;

XX WPI; 1999-190165/16.

DR P-PSDB; AAW93493.

XX New lactoferrin-binding protein B polynucleotides - obtained from  
 PT Neisseria meningitidis, used to develop products for the diagnosis,  
 prevention and treatment of neisserial disease, e.g. meningitis.

XX Claim 2; Page 82-86; 116pp; English.

XX This invention describes novel lactoferrin-binding protein B (lbpB)  
 CC strains of Neisseria meningitidis. The products of this invention can be

CC used for vaccinating humans against neisserial disease e.g. meningitis.  
CC Antibodies raised against the proteins of the invention can be used for  
CC diagnosing or treating neisserial disease in humans. The IbpB  
CC polypeptides can also be used for identifying compounds which inhibit the  
CC polypeptides  
XX  
SQ

Sequence 2169 BP; 675 A; 457 C; 550 G; 487 T; 0 U; 0 Other;

Query Match 55.3%; Score 1250.6; DB 2; Length 2169;

Best Local Similarity 76.9%; Pred. NO. 2.4e-298;

Matches 1641; Conservative 0; Mismatches 429; Indels 63; Gaps 7;

```
QY 1 ATGTGTAACCGAATTATGGCGGCAATCTCTGTGTGGCCCTTACTTTTAGCATCTTGATC 60
DB |||
QY 1 ATGTGTAACCGAATTATGGCGGCAATCTCTGTGTGGCCCTTACTTTTAGCATCTTGATC 60
DB |||
QY 61 GCGGCAATTTCCGGGTACAGCCTGTGTGCAATCAACGCCGACCGCCCACTCTGTCA 120
DB |||
QY 61 GCGGCAATTTCCGGGTACAGCCTGTGTGCAATCAACGCCGACCGCG----- 108
DB |||
QY 121 GATTCCAATCTTCAATCTCGGATAGCTGTCTCAGCTCTCTGCCGAGCCTTCGGTA 180
DB |||
QY 109 TACCCCGTCACTTTCAAGCTTAAGGACGTTCCCACTTCGCCCTTCCCGGGTCTTCGGTA 168
DB |||
QY 181 GAAATCACCGCGTCAAGCGGCCCGTTCGGTGGGCAATCGCGCTGCCAAGCGGAAT 240
DB |||
QY 169 GAAACACCGCGGTCAACAGCCCGCGTTCGGTGGGCAATCGCGCTGTGAGCGGAAT 228
DB |||
QY 241 ATCGCAACTTTTGATAAAATAGTAAATGAAATTTCCCAATAGTAAGCAGGAGGAT 300
DB |||
QY 229 ACTGCTTTTCATCGTGAAGATGGCACGGCAATTCGCCGATAGCAACAAGCAGAAAG 288
DB |||
QY 301 CTGCGCTCAAGAGAGGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB |||
QY 289 CTGTGCTTTAAAGAGGTGATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 348
DB |||
QY 361 AAACCTTAAAGGAATCAACGAGCGCATCTTAATGACCAATCTACACGTCCGATTTA 420
DB |||
QY 349 CAACCTTAAAGCGAATTCATAAGTAATCTGTAGGCAAGCATTTACCACATCGGAAT 408
DB |||
QY 421 AAAGATGATGCGTATCAATATAAATATGTCCGGCGGATATGTTTATATACTAGATGGA 480
DB |||
QY 409 GAAATATAAAATATAAATATATCGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 468
DB |||
QY 481 ACAGATGAATTCGAACAGACTCAGCGGTAGCGGTTTACCCACGCTTAGTTATGAC 540
DB |||
QY 469 AAAGATGAATTTGAGAAACATCGGATGAAAGCAGTCTTCTAATCGTTTAGGCTATGAC 528
DB |||
QY 541 GGTGTTGTATATTATTCGGGAAACGTCTTCCCAATCTTTACCGAGTCGGGAAACGGTG 600
DB |||
QY 529 GGTGTTGTATATATCTCGAGAACATCTTCCCAATCTTTACCGAGTCGGGAAACGGTG 588
DB |||
QY 601 GAATATCTGTGTAACGGCAATATATGACCGATGCGCAACGTCATCGACAGGTCAAGCG 660
DB |||
QY 589 AAATATTCGGCAACTGGCAATATATGACCGATGCGCAACGTCATCGACAGGTCAAGCG 648
DB |||
QY 661 GTTGCAATGCAATTTGGGTTATACATTTATGTTATGTTATGTTATGTTATGTTATGTT 720
DB |||
QY 649 GTTTCAGTGTGGTTTATACCATATATATGTTATGTTATGTTATGTTATGTTATGTT 708
DB |||
QY 721 TATGGGCTAAGGATGTCGACGAAAGGAAAGCATCTCGCCCAATATACGGTTGATTTT 780
DB |||
QY 709 TATGAGCTAGGATGTCGATGCGCGGAAAGCAATCTTCCCAATCTTTACCGAGTCGGG 768
DB |||
QY 781 GATAACAAACCAATGATGCAAGCTGATTAATAAATCAGTATGTGCGAATAAATAAGAT 840
DB |||
QY 769 GACAAAAAACCCTGAGGTAAGTTGATTAATAAATCAGTATGTC---AAAAGAGAGAT 825
DB |||
QY 841 GAACCCAAAAACCGCTGACATTTACGACATTTACTGCAAAATTTGACGCGCAACCGCTTT 900
DB |||
QY 826 GATCCTAAAAATCACTGACATTTTACACATTTACCGCAACATTTGACGCGCAACCGCTTT 885
DB |||
QY 901 ACCGGCAGTGCCAAAGTCAATCTGTATTTAGCGAAAAAACCCTTCCCGGTATGAGCGTTG 960
DB |||
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DB ACCGCGAGTGCCTAAGTTAGCACCGAGGTGAAGACGCAACACGCTGATAAAGAAATATTTG 945
QY TTTTTCATGCGCATGCGGATCAGCGCTTGAAGCGGCTTTTTCGGCGATTAACGAGAA 1020
DB TTTTTCATGCGCATGCGGATCAGCGCTTGAAGCGGCTTTTTCGGCGATTAACGAGAA 1005
QY GAGCTTGGCGAGCGTATTATCAGCAACGACACAGCGTATTTCGGCTATTTCGACGCA-- 1078
DB GAGCTTGGCGAGCGTATTATCAGCAACGACACAGCGTATTTCGGCTATTTCGACGCAAA 1065
QY -AAAAACAGACAGACAGCAACGACAGATACAAACCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
DB CAAAAACAGACAGACAGCAACGACATCAGATCAAACTCTGCTGCTGCTGCTGCTGCTGCT 1125
QY ACCAAATCTTGGATCTCTTAAATTTCCGTTGACGAGGCGACTGATGGCCATCCCGCT 1197
DB ACCAAATCTTGGATCTCTTAAATTTCCGTTGACGAGGCGACTGATGGCCATCCCGCT 1185
QY AAGTTTGGCATTTCTCTATGCTCCGATTTTGGTTCATCCCGCAAACTTTCTTGTGCAAGGG 1257
DB AAGTTTGGCATTTCTCTATGCTCCGATTTTGGTTCATCCCGCAAACTTTCTTGTGCAAGGG 1245
QY CGTGAATTCCTTTGGTAAACGAAACCAATCATCAAGCTTGCCTGCTGCTGCTGCTGCTGCT 1317
DB CGTGAATTCCTTTGGTAAACGAAACCAATCATCAAGCTTGCCTGCTGCTGCTGCTGCTGCT 1305
QY ACCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377
DB ACCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1365
QY CGCCCGCGCAAGTAAACCAAGCGGAGATTAAGCGGAGGATGAAGAGGTCGACGCGTT 1437
DB CGCCCGCGCGTCAACCGGACGCGAGGATGAAGAGGATTCGACATTTGATTAATGCGGAA 1425
QY GATAACGACGAAAGAAA---GCGAAGACGAGCGGTAGAAAGCAGAGCGGCGGCAAGAGAC 1494
DB GAAAGCGAAGACGAAATTTCCGAGATGATACGCGGAGATGAAGTCAACCGGAAAGAG 1485
QY GAAACT-----TCCGAGAGGATTAAGCGGAGACGAGCAACCGCCGAAAGAGAA 1548
DB GAAGCTGAAGAACCGAAGAGAAACTGATGAAGACGAGAGAGAGAACCCCGAGAAACT 1545
QY ACCGAAAGAGTGTGTAAGCCGAGAGGAGGAGGTTGAAAGACCCGCAAGAAATATCGCG 1608
DB GAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAAATCGCG 1605
QY ---GAGAAAGGCAACGCGGTTTCAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665
DB ACAGAAAGAGGCAACGCGGTTTCAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665
QY AGGACATCGACCTTTCTGAAAGGTATCCGACGCGCAACGATATTCGCAAGATTCGCGAAAGC 1725
DB AGGACATCGACCTTTCTGAAAGGTATCCGACGCGCAACGATATTCGCAAGATTCGCGAAAT 1725
QY GGAAGCGGCAATATACCGGCACTTTGGGAGGCGGTTATCGGCAACCCATTCATATGGGAC 1785
DB GGAAGCGGCACTATACCGGCACTTTGGGAGGCGGTTATCGGCGTCCGCGATGAAGAGG 1785
QY AATCAGCGCGATG-----AAAAGCGGCAAA 1812
DB GAACGCTAGATGGCACTACGTCCTCAATTCAAAAGGATAGTATGCGAATCAAGCGGCAAA 1845
QY GCAGAAATTTACCGTTGATTTGCAAGAAATCGATTTCCGAAAGCTGACGAGGCAAAAC 1872
DB GCAGAAATTTGACGTTGATTTGTCGAAAGTCTGCTTTCAGTTAGTTGACAGAAAT 1905
QY GCGTAGAACCTGCTTTTCCATATTAAGACGCGCAAGATTCATGGCAACCGTTTCCAGCG 1932
DB GATACACACCCCGCTTTTATATTTGAAAAGGTTGATTTGATGGCAACCGTTTCCAGCT 1965
QY ACAGCGGCACTCGGAGAGCGGCATCAATCTTTTCGGGAAATCTTTTCGACCGACCCCAAA 1992
DB |||
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Db 1966 TTGGCGGCTACTCGTGAATAATGGTGTGATTGTTCTGGCGAAGGTTGACATAATCCCAA 2025  
QY 1993 ACATTCCAGCTAGTAATCTTCGTGTAGAGAGGATTTTACGGCCCGCAGCGCGCGGAA 2052  
Db 2026 AGTTTAAAGCGCAGTAATCTTCTCGTAGAGGAGGATTTATGGTCCGCGCGCGCAGAG 2085  
QY 2053 TTGGCGGCTACTATTTCATAAATGATGGGAAA 2085  
Db 2086 TTGGGTGTAATATATATCGACAGTGACCGGAAA 2118

## RESULT 9

AAA81482/C

ID AAA81482 standard; DNA; 14652 BP.

XX AAA81482;

XX 04-DEC-2000 (first entry)

XX N. meningitidis partial DNA sequence gnm\_30 SEQ ID NO:30.

XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;  
KW Meningococcus B; MenB; ds.  
XX Neisseria meningitidis.

OS W0200022430-A2.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US023573.

XX 09-OCT-1998; 98US-0103794P.

XX 30-APR-1999; 99US-0132068P.

XX (CHIR ) CHIRON CORP.

XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;

PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;

PI Rappuoli R, Pizza M;

XX WPI; 2000-318079/27.

XX Isolated nucleotide sequences of Neisseria meningitidis which can be used

PT in the diagnosis and treatment of N. meningitidis infection and other

PT Neisseria infections, for example, N.gonorrhoea.

XX Claim 7; Page 582-586; 1760pp; English.

XX The present invention describes methods of obtaining immunogenic proteins  
CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent  
CC specifically claimed Neisseria meningitidis genomic DNA sequences;  
CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA  
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and  
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of  
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent  
CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all  
CC used in the exemplification of the present invention. The nucleic acid  
CC sequences, protein sequences, and antibodies against them, can be used in  
CC the manufacture of a composition. The composition can be used as a  
CC medicament (or in the manufacture of a medicament) for treating,  
CC preventing or diagnosing infection due to Neisseria bacteria. For  
CC example, some of the identified proteins could be components of vaccines  
CC against Meningococcus B; against all serotypes; and/or against all  
CC pathogenic Neisseriae. Identification of sequences from the bacterium  
CC will also facilitate production of biological probes, particularly  
CC organism-specific probes. Attempts to make efficacious Meningococcus B  
CC vaccines have failed mainly due to antigen tolerance. Multivalent  
CC vaccines have also been tried but none have successfully overcome  
CC antigenic variability. The provision of further, complete sequences may  
CC provide an opportunity to identify secreted or surface exposed proteins  
CC that may be presumed targets for the immune system and which are not

CC antigenically variable or at least more conserved than other more  
CC variable regions

XX SQ Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;  
Matches 1334; Conservative 0; Mismatches 163; Indels 66; Gaps 7;

Query Match 48.6%; Score 1100.2; DB 3; Length 14652;  
Best Local Similarity 85.3%; Pred. No. 7e-261;  
Matches 1334; Conservative 0; Mismatches 163; Indels 66; Gaps 7;

QY 712 GCAACTTCTTATGCGGCTTAAGGATGTCACAAAGGAAAAAGCATCTCGCAAAATATACG 771

Db 14652 GCAACTTCTTATGAGGTAGGATGCCAGACGAGGAAAGCATCTCGCGAATATACG 14593

QY 772 GTTCAATTTGATAACAAAAACCATCAATGGCAAGCTGATTAATAAATCAATGTGCAAAAT 831

Db 14592 GTTCATTTTGATAACAAAAACCATCAATGGCAAGCTGATTAATAAATCAATGTGCAAAAT 14533

QY 832 AAAA-----AAGATGAACCCAAAAACCGCTGACCATTTACGACATTTACGCAAAATG 885

Db 14532 AAAAGTAATCCAAATGAGCCCAAAAAACCGCTGACCATTTACGACATTTACGCAAAATG 14473

QY 886 GACGCCAACCGCTTTTACCGGCAGTGCCCAAGTCAATCTGATTTTAGCGAAAAAATCTGCC 945

Db 14472 GACGCCAACCGCTTTTACCGGCAGTGCCCAAGTCAATCTGATTTTAGCGAAAAAATCTGCC 14413

QY 946 GGTAAATGAGCGTTTGTGTTTCCATGCCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTC 1005

Db 14412 GATAAAGATATATTTGTTTCCATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTC 14353

QY 1006 GCGGATAACGAGAGAGCTTGCGGAGCGGTTTATCAGCAACGACCAACAGCGGTATTCGGC 1065

Db 14352 GCGGATAACGAGAGAGCTTGCGGAGCGGTTTATCAGCAACGACCAACAGCGGTATTCGGC 14293

QY 1066 GTATTCGACGCA-----AAAAAACAAGACAGCAACAAACGACAGATACAAAACCTGCCCTG 1122

Db 14292 GTATTCGACGCAACCAAAAAACAAGACAGCAACAAACGACAGATACAAAACCTGCCCTG 14233

QY 1123 CCGTCTGGAAAAACACACCAAAATCTTGATTTCTTAAAAATTTCCGTGACGAGCGGACT 1182

Db 14232 TCGTCTGGAAAAACACACCAAAATCTTGATTTCTTAAAAATTTCCGTGACGAGCGGACT 14173

QY 1183 GATGCCCATGCCGCTAGTTTGGCAATTTCTCTATGCCCGATTTTGTCTATCCCGCAAA 1242

Db 14172 GATAAAATCCCGCTAGTTTGGCAATTTCTCTATGCCCGATTTTGTCTATCCCGCAAA 14113

QY 1243 CTCTCTGCAAGGCGGTGAAATTTCTTGGTAAACGAAAGCAAAATCATCAAGCTTGCC 1302

Db 14112 CTCTCTGCAAGGCGGTGAAATTTCTTGGTAAACGAAAGCAAAATCATCAAGCTTGCC 14053

QY 1303 GACGCAAGAAATGACCGCTCGGTGTTGTGGACTTTTGTGACCTATGTGAAACTCGGA 1362

Db 14052 GATGGTAGGAAAAACGACAAATCCGAACTCGTGGGATTTTCTGACCTATGTGAAACTCGGA 13993

QY 1363 CGGATAAACCAGCATCCCGCGCAAGTAAACCAAGCGGCAAGATTAAGGGAGATGAA 1422

Db 13992 CGGATAAACCAGCATCCCGCGCAAGTAAACCAAGCGGCAAGATTAAGGGAGATGAA 13933

QY 1423 GAGGCTGACGCGCTTGATAACGACGAAAGGCGAAGACGAAAGCGTAGAAGACGAGGC 1482

Db 13932 GAGGATAACGCGCTTGATAGCTCGAAGAGGCGGCAAGACGAAATCGACATGAGAGGC 13873

QY 1483 GCGGAGAGACGAAACTTCCGAAAGAGGATPAATGGCGAAGACGAAAGCAACCGCGAA 1542

Db 13872 ACCGAAAGACG-----CAGCGGTAAAGACGAAAGGACGAAAGAA 13834

QY 1543 GAGGAAACGAGAGAGTTGATGAGCCGAGAGGAGAGAGTGTGAAGACCGGAGAA 1602

Db 13833 GACGAGCGGTAGAGGT-----GAGATGAAGCTGAAGAACCCCGAAGAGAA 13786

QY 1603 TCGCCCG---GCAGAGGCGAACCGCGGTTCAGGCGAGCATCTGCTGCCCTTAGAGCTCT 1659

Db 13785 TCGCCCGAGAGAGAGCGGCGAGCGGTTCAGGCGAGCATCTGCTGCCCTTAGAGCTCT 13726



QY 1639 CTGCTGCCCTAGAGCCTCTAAGGCGAGGACATCGACCTTTTCTGTGAAGGTATCCGC 1698  
Db 394 CTGCTGCCCTCGGAAGCCTTAAGGCGAGGACATCGACCTTTTCTGTGAAGGTATCCGC 453  
QY 1699 ACGGCGAAGACGGATATTCGCGAAGCGGAAACCGGCGCATATATACCGGCATCTGGGAAGCG 1758  
Db 454 ACGGCGAAGACGGATATTCGCGAAGCGGAAACCGGCGCATATATACCGGCATCTGGGAAGCG 513  
QY 1759 CGTATCGGCAAAACCCATTCAATCGGCAATCGAGCGGATCAAAAGCGGCAAAAGCAGAA 1818  
Db 514 CGTATCGGCAACCCATTCAATCGGCAATCGAGCGGATCAAAAGCGGCAAAAGCAGAA 573  
QY 1819 TTTACCGTGTATTCGCAAGAAATCGATTTCGCGAAGCTGACGAGCAAAACGGCGTA 1878  
Db 574 TTTACCGTGTATTCGCGAAGAAATCGATTTCGCGAAGCTGACGAGCAAAACGGCGTA 633  
QY 1879 GAACCTGCTTTCATATTTGAAGCGGCAAGATGATGGCAACCGTTTCCACGCGACAGCG 1938  
Db 634 CAACCTGCTTTCATATTTGAAGCGGCAAGATGATGGCAACCGTTTCCACGCGACAGCA 693  
QY 1939 CGCACTCGGAGAGCGGCATCAATCTTTCGGAAGATGTTTCGCGCCGCGCGGCAATTTGGGC 2058  
Db 694 CGCACTCGGAGAGCGGCATCAATCTTTCGGAAGATGTTTCGCGCCGCGCGGCAATTTGGGC 812  
QY 2059 GGTACTATTTTCAATATGATGGGAAATCTCTAGTATTAATCTGAATAATTTGAAATGAA 2118  
Db 813 GGTATATTTTCAATATGATGGGAAATCTCTAGTATTAATCTGAATAATTTGAAATGAA 868  
QY 2119 GCTGAAGCTGAAGTTGAAGTTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGC 2178  
Db 869 -----TAAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGC 920  
QY 2179 AAACAGTTAGAACCTGATGAAGTTAAACACAAATTCGGCGTGGTATTCGGTSCGAAGAA 2238  
Db 921 GAACAGTTAGAACCTGATGAAGTTAAACACAAATTCGGCGTGGTATTCGGTSCGAAGAA 980  
QY 2239 GATATGAGGAGGTGGAAAA 2258  
Db 981 GATAATAAGAGGTGGAAAA 1000

RESULT 11  
ABK37769  
ID ABK37769 standard; DNA; 1000 BP.  
AC ABK37769;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE DNA sequence upstream of lbpA #1 gene.  
XX  
KW Upstream sequence; ds; Antibacterial; vaccine; bleb;  
KW Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;  
KW meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;  
KW sinusitis.  
XX  
OS Neisseria meningitidis serogroup B.  
XX  
FN WO200209746-A2.  
XX  
PD 07-FEB-2002.  
XX  
XX 31-JUL-2001; 2001WO-EP008857.  
XX  
PR 31-JUL-2000; 2000WO-EP007424.  
PR 08-FEB-2001; 2001GB-00003170.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX

PI Berthet FJ, Dalemans W, Dencel P, Dequesne G, Feron C, Garcon N;  
PI Lobet Y, Poolman J, Thiry G, Thonnard J, Voet P;  
XX WPI; 2002-188688/24.  
DR  
XX  
XX  
PT New immunogenic composition comprising an antigen derived from a pathogen  
PT and a blep preparation from Neisseria meningitidis, useful as a vaccine  
PT for treating or preventing disease caused by the pathogen.  
XX  
XX  
PS Disclosure; Page 84; 125pp; English.  
XX

CC The invention relates to an immunogenic composition comprising an antigen  
CC derived from a pathogen capable of protecting a host against the  
CC pathogen, mixed with an adjuvant comprising a bleb preparation derived  
CC from a Gram-negative bacterial strain. The immunogenic composition  
CC consists of N. meningitidis B blebs or N. meningitidis C polysaccharide  
CC antigen. The blebs (derived from the outer membrane) may also have their  
CC toxic lipopolysaccharide (LPS) content reduced using heterologous down  
CC regulating sequences for LPS pathway genes or by up regulating genes  
CC involved in LPS synthesis suppression, by a promoter replacement  
CC technique. The immunogenic preparation is useful in the manufacture of a  
CC medicament for the treatment of a disease caused by the pathogen from  
CC which the antigen is derived (e.g. from Neisseria, meningitis and  
CC bacteraemia, from Moraxella, otitis media and pneumonia, and from H.  
CC influenzae chronic bronchitis, sinusitis, pneumonia and otitis media).  
CC The bleb derived from M. catarrhalis or from a non-typeable H. influenzae  
CC is useful as an adjuvant in an immunogenic composition comprising one or  
CC more pneumococcal capsular polysaccharides or protein antigens. The  
CC present sequence is an upstream sequence from an N. meningitidis,  
CC H. influenzae or M. catarrhalis gene involved in LPS biosynthesis, which  
CC either up regulates or down regulates sequences to which it is attached  
XX

SQ Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;

Query Match 32.3%; Score 730; DB 6; Length 1000;  
Best Local Similarity 84.8%; Pred. No. 6.4e-170;  
Matches 882; Conservative 0; Mismatches 115; Indels 43; Gaps 4;  
QY 1222 GATTTTGTGTATCCGACAAATCTTCTGTGCAAGGCGGTGAATCTTTGGTAAACGAA 1281  
Db 1 GATTTTGTGTATCCGACAAATCTTCTGTGCAAGGCGGTGAATCTTTGGTAAACGAA 60  
QY 1282 GAACAAATCATCAAGCTTGCCGACGCGAGGAAATGACCGTCCGTGTTGTGGACTTT 1341  
Db 61 GAGAAAACCATCAAGCTTGCCGATGCGAGGAAATGACCGTCCGTGTTGTGGACTTT 120  
QY 1342 TTGACCTATGTGAACCTCGGACGGATAAACCGATCGCCGCGCAAGTAAACCAAGGCG 1401  
Db 121 TTGACCTATGTGAACCTCGGACGGATAAACCGATCGCCGCGCAAGTAAACCAAGGCG 180  
QY 1402 GAAGATAAAGGGGAGGATGAAGGGTGACGGGTGATACGACGAGGAGGAGGAGGAA 1461  
Db 181 GAAGATAAAGGGGAGGATGAAGGGTGACGGGTGATACGACGAGGAGGAGGAGGAA 240  
QY 1462 GAAGCGGTAGAAGACGAGCGCGAGAGAGAGAGAACTTCCGAAAGGATTAATGCGGAA 1521  
Db 241 GAAATTTCCGAGATGAAGCGGAGAGCGCGAGAAATCTGTCGAGAGAGA----- 290  
QY 1522 GACGAGAGACCAACCGCGGAGAGAGAAACCGAGAGAGTTGATCAAGCGGAGGAGGAG 1581  
Db 291 -----ACCGAAG 333  
QY 1582 GTTGAAGAACCCGATC 1638  
Db 334 GTTGAAGAACCCGATC 393  
QY 1639 CTGCTGCCCTAGAAGCCTCTAAAGCGAGGACATCGACCTTTTCTGTGAAGGTATCCGC 1698  
Db 394 CTGCTGCCCTAGAAGCCTCTAAAGCGAGGACATCGACCTTTTCTGTGAAGGTATCCGC 453  
QY 1699 ACGGCGAAGACGGATATTCGCGAAGCGGAAACCGGCGCATATATACCGGCATCTGGGAAGCG 1758  
Db 454 ACGGCGAAGACGGATATTCGCGAAGCGGAAACCGGCGCATATATACCGGCATCTGGGAAGCG 513

QY	1759	CGTATCGGCAACCAATCAATGGCAATGAGCGGATGAAAGCGGCAAGAGCAAA	1818
Db	514	CGTATCGGCAACCAATCAATGGCAATGAGCGGATGAAAGCGGCAAGAGCAAA	573
QY	1819	TTTACCGTTGATTCGACAAATCGATTTCCGGAAGCTGACGGAGCAAAACGGGTA	1878
Db	574	TTTACCGTTGATTTCCGCGAGAAATCGATTTCCGGAAGCTGACGGAGCAAAACGGGTA	633
QY	1879	GAACTGCTTTCCATATTGAAGACGGCAAGATTGATGGCAACGGTTTCCACGCAACGG	1938
Db	634	CAACTGCTTTCTATTATTGAAACGGCAAGATTGATGGCAACGGTTTCCACGCAACGG	693
QY	1939	CGCACTCGGAGAGCGGCATCAATCTTTCCGGAATGTTCCAGCCCAACCAATTC	1998
Db	694	CGCACTCGTGAAGACGGGCATCAATCTTTCCGGAATGTTCCAGCCCAACCAATTC	753
QY	1999	CAAGCTAGTATCTTCGTGTAGAGGAGGATTTACGGCCGCGAGCGCGGAATTGGC	2058
Db	754	CAAGCTAGTATCTTCGTGTAGAGGAGGATTTACGGCCGCGCA-GCGAGGAATTGGC	812
QY	2059	GCTACTATTTCAATAATGATGGGAAATCTCTTAGTATACTGAAATATTGAAATGAA	2118
Db	813	GGTATTATTTCAATAAGATGGGAAATCTCTTAGTATACTGAAATATTGAAATGAA	868
QY	2119	GCTGAAGCTGAAGTTGAAGCTGAAGCTGAAGTTGAAGTTGAAGCTGAAGTTGTC	2178
Db	869	-----TAAAGTTGAAGTTGAAGCTGAAGTTGAAGTTGAAGCTGAAGTTGTC	920
QY	2179	AAACAGTTAGACCTGATGAGTTAAACACAAATTCGGCGTGTATTGGTCGGAAGAA	2238
Db	921	GAAACAGTTAGACCTGATGAGTTAAACACCAATTCGGCGTGTATTGGTCGGAAGAA	980
QY	2239	GATATCGAGAGGTGGAAA 2258	
Db	981	GATAATAAGAGGTGGAAA 1000	
RESULT 12			
ID	AAA81815	standard; DNA; 707 BP.	
XX	AA		
AC	AA		
XX	04-DEC-2000	(first entry)	
XX	N. meningitidis	partial DNA sequence gnm_362 SEQ ID NO:362.	
XX	Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;		
XX	antigen; vaccine; diagnosis; infection; antibacterial; identification;		
XX	Meningococcus B; MenB; ds.		
XX	Neisseria meningitidis.		
XX	WO200022430-A2.		
XX	20-APR-2000.		
XX	08-OCT-1999;	99WO-US023573.	
XX	09-OCT-1998;	98US-0103794P.	
XX	30-APR-1999;	99US-0132068P.	
XX	(CHIR ) CHIRON CORP.		
XX	Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;		
XX	Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;		
XX	Rappuoli R, Pizza N;		
XX	WPI; 2000-318079/27.		
XX	Isolated nucleotide sequences of Neisseria meningitidis which can be used		
XX	in the diagnosis and treatment of N. meningitidis infection and other		

PT	Neisserial infections, for example, N.gonorrhoea.	
XX	Claim 7; Page 1606; 1760pp; English.	
XX	The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions	
XX	Sequence 707 BP; 199 A; 155 C; 178 G; 173 T; 0 U; 2 Other;	
SQ	Query Match 20.1%; Score 455.6; DB 3; Length 707;	
	Best Local Similarity 79.4%; Pred. No. 3.2e-102;	
	Matches 571; Conservative 0; Mismatches 130; Indels 18; Gaps 2;	
QY	23 GCATTGTCTTGTTCCTTACTTTTATGATCTTGTATCGGGCGCAATTCGGCGGTACAGC	82
Db	1 GCATTGTCTTGTTCCTTACTTTTATGATCTTGTATCGGGCGCAATTCGGCGGTACAGC	60
QY	83 CTGTTGTGCAATCAACGGCGAGCGCCCACTCTGTGATGATTCCTCAATCTTCTG 142	
Db	61 CTGTTGTGCAATCAACGGCGAGCGCGG-----TACCCCGTCACCTTCAATCTA 108	
QY	143 CGGATAAGCTGCTCCAGCTCTCTGCGAGCTTCGGTAGAATTCAGCGCGGTCAACGGCG 202	
Db	109 AGAGCTTCCCTCGCCCTCGCGGTCTTCGGTAGAATTCAGCGCGGTCAACGGCG 168	
QY	203 CGCGCGTGGTGGCAATCGCGCTGCCAAGCGGGAATTCGCACTTTGATAAATG 262	
Db	169 CGCGCGTGGTGGCAATCGCGCTGCCAAGCGGGAATTCGCTTCTATAAACAAGAGC 238	
QY	263 GTAAATCAATTTCCATAGTAAAGCGGAGAGGATCTGCGCTCAAGAGAAGGATA 322	
Db	229 GTACGGAAATTTCCGACAGCATCAGGAGAGGAGCATCTGCCGCTTAAGAGAAGGATA 288	
QY	323 TCCTGTTTTAGACGCTAGCTGCAAGAGAACAGCTGACAACTTAAAGGAATCAACG 382	
Db	289 TCCTGTTTTAGACGCTAGCTGCAAGAGAACAGCTGACAACTTAAAGGAATCAACG 348	
QY	383 GACGCGATCTTAATGACCAATCTACAGTCCGATTTAAAGATGATCGGTATCAATATA 442	
Db	349 AACGGTATTTCTGATGTGAGGGTTATCACATCGAAAAAAGAGAATAATATCAATATC 408	
QY	443 AATATGTCGGCGCGGATATGTTTACTAGATATGCAACAG-----ATGAAATCGAAC 496	
Db	409 AATTTGTCGGTGGGCTATGTTTACAGGGCGGAGGAGGAATGAAAGAGAA 468	
QY	497 AGAACTCAGCGGGTAAAGCGGGTTACCCACCGCTTATGAGGTTTGTATATTT 556	
Db	469 AGACTTCTGATGTGAGGAGTTGTTTAAACCGATTAAGTTATGACGGTTTGTATATTT 528	
QY	557 CCGGAGAAACGTCCTTCCCAATCTTACCGAGTGGGGAACGGTGGATATTTCTGTTACT 616	



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Db      529  CCGGAGAACGTCCTCTCCCAATCTTTACCGAGCGGGAAAGGTGCATATTCGGTAACT 588
QY      617  GGCAATATATGACCGATGCCAAAGCTCATCGAGCGTCAAGCGGTGGCAATTCACAAT 676
Db      589  GGCATATATATGACCGATGCCAAAGCTCATCGAGCGGTCAAGCGGTGGCAATTCACAAT 648
QY      677  TGGGTTATATACATATTTATGTTAAGCATCTGTCGCACTCTTATGCGGCTTAAGAT 735
Db      649  TGGGTTATACCATATATGTTAAGCATCTGTCGCACTCTTATGCGGCTTAAGAT 707

RESULT 13
ABS67377
ID      ABS67377 standard; DNA; 3300 BP.
XX
AC      ABS67377;
XX
DT      29-NOV-2002 (first entry)
XX
Neisseria gonorrhoeae lbpA gene.
DE
KW      Gram-negative bacterial bleb; PorB; outer membrane protein;
KW      Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
KW      protective antigen; antibacterial; vaccine; gene; ds.
XX
OS      Neisseria gonorrhoeae.
XX
PN      WO200262380-A2.
XX
PD      15-AUG-2002.
XX
PF      08-FEB-2002; 2002WO-EP001356.
XX
PR      08-FEB-2001; 2001GB-00003169.
XX
PA      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI      Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;
XX
WPI; 2002-657510/70.
DR      P-PSDB; ABG31056.
XX
Novel gram-negative bacterial bleb presenting on its surface PorB outer
membrane protein from Chlamydia trachomatis or protective antigen from
Chlamydia pneumoniae, useful for preventing Chlamydia infection.
XX
PS      Disclosure; Page 48-49; 75pp; English.
XX
The present invention relates to a new gram-negative bacterial bleb
presenting on its surface the PorB outer membrane protein from Chlamydia
trachomatis, or a protective antigen from C. pneumoniae. The invention is
useful for preventing C. trachomatis or C. pneumoniae infection in a
host. The present nucleic acid sequence represents a Neisseria
gonorrhoeae gene as described in the invention
XX
SQ      Sequence 3300 BP; 897 A; 807 C; 921 G; 675 T; 0 U; 0 Other;
Query Match          7.5%; Score 169.2; DB 6; Length 3300;
Best Local Similarity 77.5%; Pred. No. 3.1e-31;
Matches 248; Conservative 0; Mismatches 33; Indels 39; Gaps 2;

QY      1943 CTGGGAGAGCGGCATCAATCTTTCGGGAATGTTTCGACCGACCCCAAAACATTCGAAG 2002
Db      1 CTGGGATACCGCATCAATCTTTCGGGAATGTTTCGACATAATCTCTCAAAGTTTCAAAG 60
QY      2003 CTAGTAATCTTCGTAGAGGAGGATTTTACGCCCGGAGCGCGGATTCGGCGGTA 2062
Db      61 CCAGCAATCTCTTGTAAACGGCGGCTTTTACGCCCGGAGCGCGGATTCGGCGGCA 120
QY      2063 CTATTTTCAATATGATGGGAATCTCTTAGTATAACTGAAAATATTGAAAATGAAGCTG 2122
Db      121 CTATTTTCAATAGGATGGGAATCTCTTGTATTAATCTGAAGATATTGAAA----- 172
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QY      2123 AAGCTGAAGTTGAAGTTGAAGCTGAAGCTGAAGTTGAAGTTGAAGCTGATTTGGCAAAC 2182
Db      173 -----TGAAGTTGAAATGAAGCTGATTTGGCGAAC 204
QY      2183 AGTTAGAACTGATGAAGTTAAACACAAATTCGCGCTGGTATTTCGGTGCCAGAAAGATA 2242
Db      205 AGTTAGAACCC---TGAAGTTAAACCCCAATTCGCGCTGGTATTTCGGTGCCAGAAAGATA 261
QY      2243 TGCAGAGAGGTGGAATAATGA 2262
Db      262 ATAAAGAGGTGGAATAATGA 281

RESULT 14
AAS68580
ID      AAS68580 standard; cDNA; 963 BP.
XX
AC      AAS68580;
XX
DT      13-FEB-2002 (first entry)
XX
DNA encoding novel human diagnostic protein #4384.
DE
KW      Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW      food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS      Homo sapiens.
XX
PN      WO200175067-A2.
XX
PD      11-OCT-2001.
XX
PF      30-MAR-2001; 2001WO-US008631.
XX
PR      31-MAR-2000; 2000US-00540217.
XX
PR      23-AUG-2000; 2000US-00649167.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Drmanac RT, Liu C, Tang YT;
XX
WPI; 2001-639362/73.
DR      P-PSDB; ABG04393.
XX
New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity.
XX
Claim 1; SEQ ID NO 4384; 103pp; English.
XX
The invention relates to isolated polynucleotide (I) and polypeptide (II)
sequences. (I) is useful as hybridisation probes, polymerase chain
reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
polypeptide in tissue, as molecular weight markers and as a food
supplement. (II) and its binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful for treating disorders
involving aberrant protein expression or biological activities. The
polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
coding sequences of the invention. Note: The sequence data for this
patent did not appear in the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
```

```
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities in
CC polypeptide and polynucleotide sequences have application as
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
xx
SQ Sequence 400 BP; 215 A; 34 C; 131 G; 19 T; 0 U; 1 Other;
Query Match 4.4%; Score 99.2; DB 5; Length 400;
Best Local Similarity 59.4%; Pred. No. 2.6e-14;
Matches 167; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
QY 1383 GGCAGTAAACCAACGCGGAGCATTAACGGGAGGATGAAGAGGTGTCAGCGCTTGATAA 1442
DB 120 GGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 179
QY 1443 CGACGAAAGAACGGAAGACGAACCGCTTAGAAGACGAAGCGCGCGAAGAGACGAACCTTC 1502
DB 180 AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 239
QY 1503 CGAAGAGGATAATTGGCGAAGACGAAGACACCGCCGAAGAGAAACCGAAGACTTGA 1562
DB 240 GGAAGCGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 299
QY 1563 TGRAGCCGAAGAGGAGGAAGCTTCAAGAACCCGAAGAAAATCCCGCGAAGAGGCAACGG 1622
DB 300 AGAAGAAGAAGAAGAAGAAGGGAAGACACTGAGTTAACAGSGCTGCCCCAGGCTCAGA 359
QY 1623 CGGTTTCAGGCGAGCATCTCGCTTCCTTAGAAGCCTCTTAAG 1663
DB 360 CAGGACCAGATAGACCTGGAGGATCCACAAGCTGGCCAAG 400
Search completed: August 24, 2004, 14:38:28
Job time : 777.365 secs
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Search completed: August 24, 2004, 14:38:28  
Job time : 777.365 secs

[illegible]

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 12:38:10 ; Search time 164.35 Seconds  
(without alignments)  
7637.968 Million cell updates/sec

Title: US-10-735-098-7  
Perfect score: 2262  
Sequence: 1 atgtgtaaacgaattatgg.....tcgaggagggtggaataatga 2262

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
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3: /cgn2\_6/prodata/2/ina/6A COMB.seq\*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq\*  
5: /cgn2\_6/prodata/2/ina/PCUS COMB.seq\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	90.6	4.0	7218	1	US-08-232-463-14
C 2	86.2	3.8	929	4	US-09-671-317-14
C 3	86.2	3.8	1001	4	US-09-671-317-14
C 4	84.6	3.7	43795	3	US-08-742-185-101
C 5	83.6	3.7	3211	2	US-08-574-959A-8
C 6	83.6	3.7	3211	3	US-09-357-014-8
C 7	83.6	3.7	3901	2	US-08-574-959A-6
C 8	83.6	3.7	3901	3	US-09-357-014-6
C 9	77.6	3.4	390	3	US-09-197-649-7
C 10	77.4	3.4	2230	3	US-08-448-194-7
C 11	77.4	3.4	2230	4	US-08-867-921-7
C 12	73.6	3.3	3489	2	US-08-728-323A-1
C 13	73.6	3.3	3489	4	US-09-298-568-1
C 14	73.6	3.3	3489	4	US-08-410-399-1
C 15	73.6	3.3	32207	2	US-08-770-379-20
C 16	73.6	3.3	32207	3	US-08-757-669A-20
C 17	73.6	3.3	32207	4	US-09-230-371A-20
C 18	70.8	3.1	966	2	US-08-766-738-2
C 19	70.8	3.1	966	4	US-09-282-610-2
C 20	70.4	3.1	1276	3	US-09-177-325-2
C 21	70.4	3.1	1276	3	US-09-411-812A-2
C 22	70.4	3.1	1276	4	US-09-590-113-2
C 23	70.2	3.1	1277	1	US-08-676-967-2
C 24	70.2	3.1	1277	1	US-08-676-974-2
C 25	70.2	3.1	1277	2	US-09-098-487-2
C 26	67.6	3.0	58909	4	US-09-596-002-30
C 27	67	3.0	1584	1	US-07-667-276A-1

C 28	66.4	2.9	16442	3	US-08-781-891-208
C 29	66.4	2.9	16442	4	US-09-618-166-208
C 30	65.8	2.9	2223	1	US-08-257-073-4
C 31	65	2.9	696	3	US-09-461-697-193
C 32	65	2.9	699	3	US-09-461-697-191
C 33	65	2.9	717	3	US-09-461-697-189
C 34	65	2.9	774	3	US-09-461-697-187
C 35	65	2.9	819	3	US-09-461-697-185
C 36	65	2.9	1669	3	US-09-461-697-184
C 37	64.6	2.9	2518	3	US-09-433-699-3
C 38	64.4	2.8	243	1	US-08-182-175A-56
C 39	64.4	2.8	243	1	US-08-474-633A-74
C 40	64.4	2.8	243	4	US-08-823-771-74
C 41	64.4	2.8	243	5	PCT-US92-06412-56
C 42	63.2	2.8	7295	2	US-08-487-826B-15
C 43	63	2.8	2295	1	US-08-375-300-3
C 44	63	2.8	2295	3	US-09-177-431-3
C 45	63	2.8	2295	5	PCT-US95-16930-3

## ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Hardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: PTZ9pt-Fls  
; US-08-232-463-14

Query Match 4.0%; Score 90.6; DB 1; Length 7218;

Thu Aug 26 10:18:17 2004

NAME/KEY: primer\_bind  
LOCATION: 139..158  
OTHER INFORMATION: upstream amplification primer  
NAME/KEY: primer\_bind  
LOCATION: 634..652  
OTHER INFORMATION: downstream amplification primer, complement  
NAME/KEY: misc binding  
LOCATION: 489..513  
OTHER INFORMATION: 12-454-363 potential probe  
NAME/KEY: misc feature  
LOCATION: 674..679,881..882,892..893  
OTHER INFORMATION: n=a, g, c or t  
US-09-671-317-14

Query Match 3.8%; Score 86.2; DB 4; Length 929;

Best Local Similarity 64.8%; Pred. No. 7.8e-13;  
Matches 138; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

QY 1391 AACCAAGCGCGAAGATAAAGGGGAGGATGAAGAGGGTGCAGCGCTTGTATACGACGAG 1450  
Db 878 ATCTCAAG 819  
QY 1451 AAAGCGAAGACCAAGCCGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1510  
Db 818 AAGAAG 759  
QY 1511 ATAATGGCGAAGCAAG 1569  
Db 758 AAGAAG 699  
QY 1570 GAAGAGGAG 1602  
Db 698 GAAGAAG 666

RESULT 3

US-09-671-317-439/c

; Sequence 439, Application US/09671317

; Patent No. 6528260

; GENERAL INFORMATION:

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; APPLICANT: Bougueleret, Lydie

; APPLICANT: Cohen, Annick

; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

; FILE REFERENCE: 62.US3.CIP

; CURRENT APPLICATION NUMBER: US/09/671,317

; CURRENT FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US 09/536,178

; PRIOR FILING DATE: 2000-03-23

; PRIOR APPLICATION NUMBER: PCT/IB00/00403

; PRIOR FILING DATE: 2000-03-24

; PRIOR APPLICATION NUMBER: US 60/126,269

; PRIOR FILING DATE: 1999-03-25

; PRIOR APPLICATION NUMBER: US 60/131,961

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 977

; SOFTWARE: Patent.pm

; SEQ ID NO 439

; LENGTH: 1001

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 501

; OTHER INFORMATION: 12-454-242 : deletion AT

; NAME/KEY: misc binding

; LOCATION: 481..500

; OTHER INFORMATION: 12-454-242.misl, potential

; NAME/KEY: primer\_bind

; LOCATION: 260..279

; OTHER INFORMATION: upstream amplification primer

; NAME/KEY: primer\_bind

; LOCATION: 502..521

; OTHER INFORMATION: 12-454-363.misl, potential complement

RESULT 2

US-09-671-317-14/c

; Sequence 14, Application US/09671317

; Patent No. 6528260

; GENERAL INFORMATION:

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; APPLICANT: Bougueleret, Lydie

; APPLICANT: Cohen, Annick

; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

; FILE REFERENCE: 62.US3.CIP

; CURRENT APPLICATION NUMBER: US/09/671,317

; CURRENT FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US 09/536,178

; PRIOR FILING DATE: 2000-03-23

; PRIOR APPLICATION NUMBER: PCT/IB00/00403

; PRIOR FILING DATE: 2000-03-24

; PRIOR APPLICATION NUMBER: US 60/126,269

; PRIOR FILING DATE: 1999-03-25

; PRIOR APPLICATION NUMBER: US 60/131,961

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 977

; SOFTWARE: Patent.pm

; SEQ ID NO 14

; LENGTH: 929

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 501

; OTHER INFORMATION: 12-454-363 : polymorphic base A or G

; NAME/KEY: misc binding

; LOCATION: 481..500

; OTHER INFORMATION: 12-454-363.misl, potential

; NAME/KEY: misc binding

; LOCATION: 502..521

; OTHER INFORMATION: 12-454-363.misl, potential complement

; LOCATION: 755..773  
; OTHER INFORMATION: downstream amplification primer, complement  
; NAME/KEY: misc feature  
; LOCATION: 795..800  
; OTHER INFORMATION: n=a, g, c or t  
US-09-671-317-439

Query Match 3.8%; Score 86.2; DB 4; Length 1001;  
Best Local Similarity 64.8%; Pred. No. 8.1e-13;  
Matches 138; Conservative 0; Mismatches 74; Indels 1; Gaps 1;  
QY 1391 AACCAAGGCGGAGATTAAGGGGAGGATGAAGAGGTCAGGCGTTGATAACGCAAG 1450  
Db 999 ATCTCAAG 940  
QY 1451 AAAGCGAAGACGAGCGCTAGACGACGAGCGCGCGGAGAGAGAGAGAGAGAGAG 1510  
Db 939 AAG 880  
QY 1511 ATATGCGGAG 1569  
Db 879 AAGAAG 820  
QY 1570 GAAG 1602  
Db 819 GAAG 787

RESULT 4  
US-08-742-185-101  
; Sequence 101, Application US/08742185  
; Patent No. 6020476  
; GENERAL INFORMATION:  
; APPLICANT: Page, David C.  
; APPLICANT: Reijo, Renee  
; APPLICANT: Saxena, Richa  
; APPLICANT: Hawkins, Trevor  
; APPLICANT: Reeve, Mary Pat  
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/742,185  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/690,734  
; FILING DATE: 31-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/310,429  
; FILING DATE: 22-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: WHI94-07A2  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43795 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-742-185-101

Query Match 3.7%; Score 84.6; DB 3; Length 43795;  
Best Local Similarity 61.6%; Pred. No. 1.2e-11;  
Matches 135; Conservative 0; Mismatches 84; Indels 0; Gaps 0;  
QY 1386 AAGTAAACCAAGCGGAGAGATTAAGGGGAGGATGAAGAGGTCAGGCGTTGATAACGA 1445  
Db 38932 AAAAAAAAAAAAAAAAAAG 38891  
QY 1446 CGAAGAAAGCGAAGACGAGCGCTAGAGAGAGAGCGCGCGGAGAGAGAGAGAGAGAGAG 1505  
Db 38892 AGGAGATGAG 38951  
QY 1506 AGAGGATTAATGCGGAG 1565  
Db 38952 GAAGGAGAGCGGAG 39011  
QY 1566 AGCGGAG 1604  
Db 39012 AGAAG 39050

RESULT 5  
US-08-574-959A-8  
; Sequence 8, Application US/08574959A  
; Patent No. 5962224  
; GENERAL INFORMATION:  
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi  
; APPLICANT: and Jack L. Strominger  
; TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/574,959A  
; FILING DATE: 19-DEC-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: DFN-008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3211 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 439..3157  
US-08-574-959A-8

Query Match 3.7%; Score 83.6; DB 2; Length 3211;  
Best Local Similarity 63.4%; Pred. No. 6.7e-12;  
Matches 128; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1457 AAGACGAGCCGTAGAGACGAAGCGCGCGAAGACGAACTTCCGAGAGGATAATG 1516  
Db 2465 AGGAGAGAGAGGAGAGAGAGAGAGACTTTTGGAGGAGAGGAGATGAAGAGGAATATT 2524  
QY 1517 GCGAAGACGAGAGAGACCAACCGCCGAGAGAAACCGGAGAGAGTTGATGACGCGCAAGAGG 1576  
Db 2525 TTGAGAGGAGAGAGAGAGAGAGAGTTTGGAGGAGAGATTTGAGGAGAGAGAGGTG 2584  
QY 1577 AGGAGTTGAGAGACCCGAGAG 1598  
Db 2585 AGTTAGAGAGAGAGAGAGAG 2606

RESULT 7

US-08-574-959A-6  
; Sequence 6, Application US/08574959A  
; Patent No. 5962224  
; GENERAL INFORMATION:  
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi  
; APPLICANT: and Jack L. Strominger  
; TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/574,959A  
; FILING DATE: 19-DEC-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragoras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: DFN-008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3901 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 439..3847  
; US-08-574-959A-6

Query Match 3.7%; Score 83.6; DB 2; Length 3901;  
Best Local Similarity 63.4%; Pred. No. 7.3e-12;  
Matches 128; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1397 AGCGGAGATATAAGGGGAGGATGAAGAGGTGCGAGCGTTGATACGACGAGAGAGCG 1456  
Db 3095 AGGAGGAGAGAGGAG 3154  
QY 1457 AAGACGAGCCGTAGAGACGAAGCGCGCGGAGAGAGAACTTCCGAGAGGATAATG 1516  
Db 3155 AGGAG 3214  
QY 1517 GCGAG 1576  
Db 3215 TTGAG 3274

QY 1397 AGCGGAGATATAAGGGGAGGATGAAGAGGTGCGAGCGTTGATACGACGAAGAGAGCG 1456  
Db 2405 AGGAGGAG 2464  
QY 1457 AAGACGAGCCGTAGAGACGAAGCGCGCGGAGAGAGAGAACTTCCGAGAGGATAATG 1516  
Db 2465 AGGAGAGAGAGAGAGAGAGAGAGAGACTTTTGGAGGAGAGAGAGAGGATGAAGAGGAATATT 2524  
QY 1517 GCGAAGACGAGAGAGACCCCGGAGAGAGAAACCGGAGAGAGTTGATGACGCGCAAGAGG 1576  
Db 2525 TTGAGAGGAGAGAGAGAGAGAGAGAGTTTGGAGGAGAGATTTGAGGAGAGAGAGGTG 2584  
QY 1577 AGGAGTTGAGAGACCCGAGAG 1598  
Db 2585 AGTTAGAGAGAGAGAGAGAG 2606

RESULT 6

US-09-357-014-8  
; Sequence 8, Application US/09357014  
; Patent No. 6291645  
; GENERAL INFORMATION:  
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi  
; APPLICANT: and Jack L. Strominger  
; TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/357,014  
; FILING DATE: 19-Jul-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/574,959  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragoras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: DFN-008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3211 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 439..3157  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
; US-09-357-014-8

Query Match 3.7%; Score 83.6; DB 3; Length 3211;  
Best Local Similarity 63.4%; Pred. No. 6.7e-12;  
Matches 128; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1397 AGCGGAGATATAAGGGGAGGATGAAGAGGTGCGAGCGTTGATACGACGAGAGAGCG 1456  
Db 2405 AGGAG 2464





Thu Aug 26 10:18:17 2004

1913 ATGCGCAACGGTTTCCACGCGACGCGGCGACTCGGGAGAGCGGCATCAATCTTTCGGGAA 1972  
1927 AGGCGCAACGGCTTTGAAGGTACGCGGAAAACCTGCTGAGTCAGGTTTGTATCTCGATCAA 1986  
1973 ATGTTTCGACCGACCCCAACATTCAGCTAGTATCTTCGTGTAGAGGAGGATTTT 2032  
1987 AAAATACCAACCGCGCACGCTTAAGGCATATATCAAGATGCCAAGTAAAGGCGGTTT 2046  
2033 ACGGCGCGGAGCGCGGAAATTTGGCGGTACTATTTTCAATAATGATGGGAA 2085  
2047 ACGGCGCTTAAGCGCAAGAGTTGGCGGATGTTTGGCTATCCGCGCGATAAA 2099  
RESULT 11  
US-08-867-921-7  
Sequence 7, Application US/08867921  
Patent No. 6326350  
GENERAL INFORMATION:  
APPLICANT: JACOBS, Eric  
APPLICANT: LEGRAN, Michele  
APPLICANT: MAZARIN, Veronique  
APPLICANT: BOUCHON-THIESEN, Bernadette  
APPLICANT: SCHRYVERS, Anthony B.  
APPLICANT: BLOCH, Marie-Aline  
TITLE OF INVENTION: DNA FRAGMENTS CODING FOR THE TRANSFERRIN  
TITLE OF INVENTION: RECEPTOR OF NEISSERIA MENINGITIDIS  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,921  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/445,472  
FILING DATE: 22-MAY-1995  
APPLICATION NUMBER: US 08/361,469  
FILING DATE: 22-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,053  
FILING DATE: 18-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 92 07493  
FILING DATE: 19-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm K.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 016100-004  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2230 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORGANISM: DNA which encodes Tbp2 subunit of transferrin  
ORGANISM: receptor

ADDRESSER: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,194  
FILING DATE: 23-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/361,469  
FILING DATE: 22-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,053  
FILING DATE: 18-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 92 07493  
FILING DATE: 19-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm K.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 016100-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2230 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORGANISM: DNA which encodes Tbp2 subunit of transferrin  
ORGANISM: receptor  
STRAIN: Neisseria meningitidis IM2169  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 60..119  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 120..2192  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 60..2192  
US-08-448-194-7  
Query Match 3.4%; Score 77.4; DB 3; Length 2230;  
Best Local Similarity 52.8%; Pred. No. 2.4e-10;  
Matches 218; Conservative 0; Mismatches 186; Indels 9; Gaps 2;  
1679 TTTTCTCTGAAGGTATCCGACGCGCAGAAACGGATATTCGCGAAAGCGGACGCGCAT 1738  
1690 TGTTCTCCAGGCGGCTACCGATGAAAAAGAGATTCCAAACCGACCAAAACGTCGTTT 1749  
1739 ATACCGGCATTTGGGAGCGGTTATCGGCAACCCATTCATGGGCAATCAGCGCGATG 1798  
1750 ATCGGGGCTTTGTGTACGGGCATATTCGCAACGGCAAGCTGGAGCGGCATCTCTG 1809  
1799 AAAAGCGGCA-----AAACGAGATTTCAGTTGATTTTCGACAGAAATCGATTCCG 1852  
1810 ATAAAGAGGGCGGCAACGCGCGGAAATTACTGTGAATTTTCCGATAAAAAATACCG 1869  
1853 GAAAGCTACCGAGCAAAACCGCGGTAGAACCTGCTTTCCATTTGAGACGCGGAGATTG 1912  
1870 GCAAGTTAACCGCTGAAACAGGCGGCGCAACCTTTACCATT---GAGGGGAATGATTC 1926



1457 AAGACGAAGCCGTAGAACGAGGCGCGGAGAGACGAACTTCCGAAGAGGATAATG 1516  
1121 AGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGAGGAGGAGGAGC 1180  
1517 GCGAAGACGAGAGACACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1576  
1181 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 1240  
1577 AGGAGGTTGAAGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGAGCA 1636  
1241 AGGAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCA 1300

RESULT 14  
US-09-410-399-1  
; Sequence 1, Application US/09410399  
; Patent No. 6482587  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, Erle S.  
; APPLICANT: Cotter, Murray A.  
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA  
; TITLE OF INVENTION: to Genomic Host DNA  
; FILE REFERENCE: UM-03778  
; CURRENT APPLICATION NUMBER: US/09/410,399  
; CURRENT FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3489  
; TYPE: DNA  
; ORGANISM: Kaposi's sarcoma-associated herpesvirus  
US-09-410-399-1

Query Match 3.3%; Score 73.6; DB 4; Length 3489;  
Best Local Similarity 56.7%; Pred. No. 2.9e-09;  
Matches 136; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
  
QY 1397 AGGCGGAAGATAAAGCGGAGGATGAAGAGGGTGCAGGCGTTGATACGACGAGAAAGCG 1456  
Db 1061 AGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACG 1120  
QY 1457 AAGACGAAGCCGTAGAACGAGGCGCGGAGAGACGAACTTCCGAAGAGGATAATG 1516  
Db 1121 AGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACG 1180  
QY 1517 GCGAAGACGAGAGCAACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1576  
Db 1181 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 1240  
QY 1577 AGGAGTTGAAGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGAGCA 1636  
Db 1241 AGGAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCA 1300

RESULT 15  
US-08-770-379-20/c  
; Sequence 20, Application US/08770379.  
; Patent No. 5849564  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Yuan  
; APPLICANT: Bohenzky, Roy A.  
; APPLICANT: Russo, James J.  
; APPLICANT: Edelman, Isidore S.  
; APPLICANT: Moore, Patrick S.  
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED  
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.

ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,379  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 52342  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 20:  
LENGTH: 32207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-770-379-20  
  
Query Match 3.3%; Score 73.6; DB 2; Length 32207;  
Best Local Similarity 56.7%; Pred. No. 8e-09;  
Matches 136; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
  
QY 1397 AGGCGGAAGATAAAGCGGAGGATGAAGAGGGTGCAGGCGTTGATACGACGAGAAAGCG 1456  
Db 20936 AGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACG 20877  
QY 1457 AAGACGAAGCCGTAGAACGAGGCGCGGAGAGACGAACTTCCGAAGAGGATAATG 1516  
Db 20876 AGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACG 20817  
QY 1517 GCGAAGACGAGAGCAACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1576  
Db 20816 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 20757  
QY 1577 AGGAGTTGAAGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGAGCA 1636  
Db 20756 AGGAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCA 20697  
  
Search completed: August 25, 2004, 05:32:07  
Job time : 166.35 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: August 24, 2004, 23:48:06 ; Search time 1138.6 Seconds  
(without alignments)  
9777.159 Million cell updates/sec  
Title: US-10-735-098-7  
Perfect score: 2262  
Sequence: 1 atgtgttaacccaattatgg.....tcgaggagtggaataatga 2262  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3237270 seqs, 2460713050 residues  
Total number of hits satisfying chosen parameters: 6474540  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Published Applications NA:\*

Result No.	Score	Query Match	Length	ID	Description
1	2262	100.0	2262	17	US-10-735-098-7
2	1465.2	64.8	2277	17	US-10-735-098-1
3	1442.6	63.8	2226	13	US-10-282-122A-29815
4	1442.2	63.8	2226	17	US-10-735-098-5
5	1291.8	57.1	2124	17	US-10-735-098-9
6	1250.6	55.3	2169	17	US-10-735-098-3
7	730	32.3	1000	17	US-10-343-561-15
8	169.2	7.5	3300	17	US-10-467-534-80
9	100.2	4.4	31124	17	US-10-087-192-463
10	98.4	4.4	37265	13	US-10-087-192-49
11	96	4.2	374849	13	US-10-087-192-49
12	94.2	4.2	635	13	US-10-087-192-1627
13	94.2	4.2	635	16	US-10-027-632-269927
14	91.6	4.0	96596	12	US-10-052-482-70

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2262	100.0	2262	17	US-10-735-098-7
2	1465.2	64.8	2277	17	US-10-735-098-1
3	1442.6	63.8	2226	13	US-10-282-122A-29815
4	1442.2	63.8	2226	17	US-10-735-098-5
5	1291.8	57.1	2124	17	US-10-735-098-9
6	1250.6	55.3	2169	17	US-10-735-098-3
7	730	32.3	1000	17	US-10-343-561-15
8	169.2	7.5	3300	17	US-10-467-534-80
9	100.2	4.4	31124	17	US-10-087-192-463
10	98.4	4.4	37265	13	US-10-087-192-49
11	96	4.2	374849	13	US-10-087-192-49
12	94.2	4.2	635	13	US-10-087-192-1627
13	94.2	4.2	635	16	US-10-027-632-269927
14	91.6	4.0	96596	12	US-10-052-482-70

15	91	4.0	522	14	US-10-101-487-71	Sequence 71, Appl
c 16	91	4.0	530	14	US-10-101-487-73	Sequence 73, Appl
17	91	4.0	554	14	US-10-101-487-69	Sequence 69, Appl
18	91	4.0	554	14	US-10-101-487-106	Sequence 106, Appl
c 19	90	4.0	305	9	US-09-864-761-19262	Sequence 19262, A
c 20	90	4.0	496	9	US-09-864-761-2534	Sequence 2534, Ap
c 21	87.6	3.9	143899	10	US-09-972-546-15	Sequence 15, Appl
c 22	87.4	3.9	68233	16	US-10-034-650-31	Sequence 31, Appl
c 23	86.4	3.8	39443	16	US-10-085-117-313	Sequence 313, App
c 24	86.2	3.8	929	13	US-10-294-934-14	Sequence 14, Appl
c 25	86.2	3.8	1001	13	US-10-294-934-439	Sequence 439, App
c 26	86.2	3.8	96602	16	US-10-085-117-61	Sequence 61, Appl
c 27	85.8	3.8	115223	17	US-10-322-281-773	Sequence 773, Appl
c 28	85	3.8	45980	10	US-09-957-956-6	Sequence 6, Appl
c 29	85	3.8	96597	12	US-10-052-482-103	Sequence 103, App
c 30	84.6	3.7	276	9	US-09-864-761-20595	Sequence 20595, A
c 31	84.6	3.7	1848	13	US-10-027-632-98794	Sequence 98794, A
c 32	84.6	3.7	1848	13	US-10-027-632-98795	Sequence 98795, A
c 33	84.6	3.7	1848	16	US-10-027-632-98794	Sequence 98795, A
c 34	84.6	3.7	1848	16	US-10-027-632-98795	Sequence 98794, A
c 35	84.6	3.7	32069	15	US-10-004-113-7	Sequence 98795, A
c 36	84.6	3.7	96595	12	US-09-997-722-43	Sequence 7, Appl
c 37	84.2	3.7	438	9	US-09-864-761-4988	Sequence 43, Appl
c 38	83.6	3.7	3120	13	US-10-112-944-191	Sequence 4988, Ap
c 39	83.6	3.7	122859	13	US-10-087-192-37	Sequence 191, App
c 40	82.6	3.7	193853	13	US-10-087-192-1663	Sequence 37, Appl
41	82.4	3.6	225883	15	US-10-087-192-1663	Sequence 1663, Ap
42	82	3.6	551	15	US-10-175-523-57	Sequence 57, Appl
43	82	3.6	927	16	US-10-029-386-5590	Sequence 57, Appl
c 43	82	3.6	927	16	US-10-369-493-26106	Sequence 5590, Ap
c 44	82	3.6	1032	16	US-10-369-493-26106	Sequence 26106, A
c 45	82	3.6	3818	13	US-10-369-493-26107	Sequence 26107, A
	82	3.6	3818	13	US-10-112-944-663	Sequence 663, App

ALIGNMENTS

RESULT 1  
US-10-735-098-7  
Sequence 7, Application US/10735098  
Publication No. US20040131634A1  
GENERAL INFORMATION:  
APPLICANT: Pettersson-Fernholm, Annika Margareta  
APPLICANT: Tommassen, Johannes Petrus Maria  
TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein  
FILE REFERENCE: B45106C1  
CURRENT APPLICATION NUMBER: US/10735,098  
PRIOR FILING DATE: 2003-12-12  
PRIOR FILING DATE: 2000-02-15  
PRIOR FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: PCT/EP98/05117  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: GB 9717423.9  
PRIOR FILING DATE: 1997-08-15  
PRIOR APPLICATION NUMBER: GB 9805544.8  
PRIOR FILING DATE: 1998-02-05  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 2262  
TYPE: DNA  
ORGANISM: Neisseria meningitidis strain M990  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)....(2259)  
US-10-735-098-7

Query Match 100.0%; Score 2262; DB 17; Length 2262;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 2262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTGTAACCGAATATGCGGCATTTGCTTTGGCCCTTACTTTAGCATCTTGTATC 60  
DB 1 ATGTGTAACCGAATATGCGGCATTTGCTTTGGCCCTTACTTTAGCATCTTGTATC 60

QY	61	GGCGGCAATTTCCGCGTACAGCTGTTGTGCGAATCAACGCGGACCGCGCCAACTCTGTCA	120	QY	1141	AAAATCTTGGATTTCTTAAATAATTTCCGTTGACGAGCGACTGATGCCATGCCCGTAAG	1200
Db	61	GGCGGCAATTTCCGCGTACAGCTGTTGTGCGAATCAACGCGGACCGCGCCAACTCTGTCA	120	Db	1141	AAAATCTTGGATTTCTTAAATAATTTCCGTTGACGAGCGACTGATGCCATGCCCGTAAG	1200
QY	121	GATTCGAAATCTTCCAAATCTCGCGATAAGCTCTCCAGCTCTCGTCCGCGAGCCCTTCGGTA	180	QY	1201	TTTGGCCATTTCTCTATGCGCGATTTTGGTCAATCCGACAAAATCTTCTTGTGCGAAGGCGT	1260
Db	121	GATTCGAAATCTTCCAAATCTCGCGATAAGCTCTCCAGCTCTCGTCCGCGAGCCCTTCGGTA	180	Db	1201	TTTGGCCATTTCTCTATGCGCGATTTTGGTCAATCCGACAAAATCTTCTTGTGCGAAGGCGT	1260
QY	181	GAATACACGCGGTCAAGCGGCGCGCGTCCGTTGCGGCAATGCGGCTGCCAAGCGGAAT	240	QY	1261	GAATTCCTTTTGGTAAACGAAACAAATCATCAAGCTTGCAGCGGACGAAAAATGACC	1320
Db	181	GAATACACGCGGTCAAGCGGCGCGCGTCCGTTGCGGCAATGCGGCTGCCAAGCGGAAT	240	Db	1261	GAATTCCTTTTGGTAAACGAAACAAATCATCAAGCTTGCAGCGGACGAAAAATGACC	1320
QY	241	ATCGCAATCTTTGATAAATAATGTAATGAAATTCCTCAATGTAAGCAGGCGAGAGAT	300	QY	1321	GTCGCTGCTGTTGCGACTTTTGTGACCTATGTGAAAATCTCGACGGAATAAACCAGATCGC	1380
Db	241	ATCGCAATCTTTGATAAATAATGTAATGAAATTCCTCAATGTAAGCAGGCGAGAGAT	300	Db	1321	GTCGCTGCTGTTGCGACTTTTGTGACCTATGTGAAAATCTCGACGGAATAAACCAGATCGC	1380
QY	301	CTGCGCTCAAGAGAGAGATATCTGTTTGTAGACGGTACGCGGAAAGAACAGCTGAC	360	QY	1381	CCGCGAAGTAAACCAAGGCGGAAAGATTAAGGGAGGATGAAGGGTGCAGGCGTTGAT	1440
Db	301	CTGCGCTCAAGAGAGAGATATCTGTTTGTAGACGGTACGCGGAAAGAACAGCTGAC	360	Db	1381	CCGCGAAGTAAACCAAGGCGGAAAGATTAAGGGAGGATGAAGGGTGCAGGCGTTGAT	1440
QY	361	AACTTAAAGAGAAATCAACGCGCGCATCTTAATGCAACCAATCTACACGCTCCGATTTA	420	QY	1441	AACGACGAAGAAAGCGAAGACGAACCGGTAGAAGACGAAGCGGCGGAAGACGAACT	1500
Db	361	AACTTAAAGAGAAATCAACGCGCGCATCTTAATGCAACCAATCTACACGCTCCGATTTA	420	Db	1441	AACGACGAAGAAAGCGAAGACGAACCGGTAGAAGACGAAGCGGCGGAAGACGAACT	1500
QY	421	AAAGATGATGCGTATCAATATAAATATGTCGCGGCGCGATATGTTTATAGATATGGA	480	QY	1501	TCCGAAAGAGATATGCGGAAGAAGCAAGCAAGCGGCGGAGAGAAACCGAAGAGTT	1560
Db	421	AAAGATGATGCGTATCAATATAAATATGTCGCGGCGCGATATGTTTATAGATATGGA	480	Db	1501	TCCGAAAGAGATATGCGGAAGAAGCAAGCAAGCGGCGGAGAGAAACCGAAGAGTT	1560
QY	481	ACAGATGAATCGAACAGAACTCAGCGGTAAGCGGTTACCCACCGCTTAGGTTATGAC	540	QY	1561	GATGAAGCGGAGAGGAGGAAAGTTGAAGAACCGGAAAGAAATCCCGCGGAGAAAGCAAC	1620
Db	481	ACAGATGAATCGAACAGAACTCAGCGGTAAGCGGTTACCCACCGCTTAGGTTATGAC	540	Db	1561	GATGAAGCGGAGAGGAGGAAAGTTGAAGAACCGGAAAGAAATCCCGCGGAGAAAGCAAC	1620
QY	541	GCTTTTGTATATTTCCGAGAAAGCTCTTCCCAATCTTTACCGAGTCCGGAACGGTG	600	QY	1621	GCGGTTTCCGAGCAGATCTGCTGCTTCCCTAGAACCTCTAAGGCGAGGACATCGACCTT	1680
Db	541	GCTTTTGTATATTTCCGAGAAAGCTCTTCCCAATCTTTACCGAGTCCGGAACGGTG	600	Db	1621	GCGGTTTCCGAGCAGATCTGCTGCTTCCCTAGAACCTCTAAGGCGAGGACATCGACCTT	1680
QY	601	GAATATCTGGTAACTGCGAATATATGACCGATGCGGATGCGGATGCGGATGCGGAT	660	QY	1681	TTTCTGAAAGGTTATCCGCAAGGAAAGGATTTCCGCAAGGAAAGGAAAGCGGCAATTA	1740
Db	601	GAATATCTGGTAACTGCGAATATATGACCGATGCGGATGCGGATGCGGATGCGGAT	660	Db	1681	TTTCTGAAAGGTTATCCGCAAGGAAAGGATTTCCGCAAGGAAAGGAAAGCGGCAATTA	1740
QY	661	GTGCGATGCAATTTGGGTTATATCAATTTATGTTAAAGATGTTGTTGCACTTCT	720	QY	1741	ACCGGCACTTGGGAGCGGTATCGCAAAACCCATTCATGCGCAAAATCAGGCGGATGAA	1800
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QY	721	TATGCGGCTAAGCATGTCGACGAAAGGAAAGGAAAGCATCTGCCAAATATACGGTTGATTT	780	QY	1801	AAAGCGGCAAAAGCAGAAATTTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAAGCTG	1860
Db	721	TATGCGGCTAAGCATGTCGACGAAAGGAAAGGAAAGCATCTGCCAAATATACGGTTGATTT	780	Db	1801	AAAGCGGCAAAAGCAGAAATTTACCGTTGATTTCCGCAAGAAATCGATTTCCGGAAGCTG	1860
QY	781	GATAACAAACCAATGATGCGAAGCTGATTAATAATCAGTATGCGAATAAATAAAGAT	840	QY	1861	ACGAGCAAAAACCGGCTAGAACTTCCATTTCCATTTGAAGACGCGCAAGATTGATGCAAC	1920
Db	781	GATAACAAACCAATGATGCGAAGCTGATTAATAATCAGTATGCGAATAAATAAAGAT	840	Db	1861	ACGAGCAAAAACCGGCTAGAACTTCCATTTCCATTTGAAGACGCGCAAGATTGATGCAAC	1920
QY	841	GAACCCAAACCAACCGCTGACATTTACGACATTTACTGCAAAATTTGACGCAACCGGTTT	900	QY	1921	GGTTTCCACGCGACGCGGCTACTTTCGAGAGAGCGGATCAATCTTTCCGGAATGTTGTCG	1980
Db	841	GAACCCAAACCAACCGCTGACATTTACGACATTTACTGCAAAATTTGACGCAACCGGTTT	900	Db	1921	GGTTTCCACGCGACGCGGCTACTTTCGAGAGAGCGGATCAATCTTTCCGGAATGTTGTCG	1980
QY	901	ACCGGAGTCCCAAGGTCATCTGATTTAGCGAAACCTTCCGCGTATGAGCGGTTG	960	QY	1981	ACCGACCCCAAAACATTTCCAAAGCTAGTAATTTCTGTTGAGAGAGGATTTTACGCGCG	2040
Db	901	ACCGGAGTCCCAAGGTCATCTGATTTAGCGAAACCTTCCGCGTATGAGCGGTTG	960	Db	1981	ACCGACCCCAAAACATTTCCAAAGCTAGTAATTTCTGTTGAGAGAGGATTTTACGCGCG	2040
QY	961	TTTTTCCATGCGATGCGGCTTACGCGGCTTTCGCGGATTAACGGAAGAA	1020	QY	2041	CAGCGCGGAAATTTGGCGGTACTATTTTCAATAATGATGCGGAAATCTCTTAGTATAACT	2100
Db	961	TTTTTCCATGCGATGCGGCTTACGCGGCTTTCGCGGATTAACGGAAGAA	1020	Db	2041	CAGCGCGGAAATTTGGCGGTACTATTTTCAATAATGATGCGGAAATCTCTTAGTATAACT	2100
QY	1021	GAGCTTCCGAGCGGTTTATCAGCAACGACAAACAGCGTATTTCCGCGTATTTCCGAGCAAA	1080	QY	2101	GAAAAATTTCAAAATGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAG	2160
Db	1021	GAGCTTCCGAGCGGTTTATCAGCAACGACAAACAGCGTATTTCCGCGTATTTCCGAGCAAA	1080	Db	2101	GAAAAATTTCAAAATGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAG	2160
QY	1081	AAAAACAGAGACAGCAACGCGAGGATCAAAAACCTGCGCTGCGGATTCGGAACACACC	1140	QY	2161	GTTGAAGCTGATTTGGCAACAGTTAGAACTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAG	2220
Db	1081	AAAAACAGAGACAGCAACGCGAGGATCAAAAACCTGCGCTGCGGATTCGGAACACACC	1140	Db	2161	GTTGAAGCTGATTTGGCAACAGTTAGAACTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAG	2220
				QY	2221	GTATTCGTCGGAAGAGATATGACGAGGTGGAATAATGA	2262



Db 2221 GTATTCCGTCGGAAGAAAGATATGACGAGGTGGAATAAATGA 2262

RESULT 2

US-10-735-098-1  
 ; Sequence 1, Application US/10735098  
 ; Publication No. US20040131634A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pettersson-Fernholm, Annika Margareta  
 ; APPLICANT: Tommassen, Johannes Petrus Maria  
 ; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein  
 ; FILE REFERENCE: B45106C1  
 ; CURRENT APPLICATION NUMBER: US/10/735,098  
 ; PRIORITY FILING DATE: 2003-12-12  
 ; PRIOR APPLICATION NUMBER: 09/485,760  
 ; PRIOR FILING DATE: 2000-02-15  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05117  
 ; PRIOR FILING DATE: 1998-08-10  
 ; PRIOR APPLICATION NUMBER: 9717423.9  
 ; PRIOR FILING DATE: 1997-08-15  
 ; PRIOR APPLICATION NUMBER: GB 9805544.8  
 ; PRIOR FILING DATE: 1998-02-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2277  
 ; TYPE: DNA  
 ; ORGANISM: Neisseria meningitidis strain BNCV  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (100)...(2274)  
 ; US-10-735-098-1

Query Match 64.8%; Score 1465.2; DB 17; Length 2277;  
 Best Local Similarity 81.1%; Pred. No. 0;  
 Matches 1835; Conservative 0; Mismatches 343; Indels 84; Gaps 8;  
 1 ATGTGTAACCGAATATATGCGGCAATCTCTGTGTGCGCTTACTTTTACGATCTGTATC 60  
 100 ATGTGTAACCGAATATATGCGGCAATCTCTGTGTGCGCTTACTTTTACGATCTGTATC 159  
 61 GCGCGCAATTTTCGGGTACAGCCTGTGTGTAATCAAGCGCGACGCGCCCACTCTGTCA 120  
 160 GCGCGCAATTTTCGGGTACAGCCTGTGTGTAATCAAGCGCGACGCGCG----- 207  
 121 GATTCGCAATCTTCCCAATCTGCGGTAAGCCTGCTCAGCTCTGCGAGCCTTCGGTA 180  
 208 TACCCGCTCACTTTCGAAGTCTAAGGACGTTCCCACTCGCCCTGCGCAACCTTCTATA 267  
 181 GAAATACGCGCGGTCAAGCGCGCGCGCTGCTGCGGCAATGCGCTGCGCAAGCGGAAT 240  
 268 GAAATACGCGCGGTCAAGCGCGCGCGCTGCTGCGGCAATGCGCTGCGCAAGCGGAAT 327  
 241 ATCGCAACTTTTGATAAAATGTAATGAAATTTCCCAATAGTAAGCAGGACGAGCTAT 300  
 328 ACTGCTTTTCATCGTGAAGATGCGCAAGATTTCCCAATAGTAAGCAGGACGAGAAAG 387  
 301 CTGCGCTCAAGAGAGAGATATCTGTTTGAAGCGGTGCGGCAAGCAAGAGAGAGAGTAC 360  
 388 CTGCGCTTCAAGAGAGAGATATCTGTTTGAAGCGGTGCGGCAAGCAAGAGAGAGTAC 447  
 361 AAATCTTAAAGAGAGATCAAGCGCGCGCATCTTAATGCAACCAATCTACGTCGATTA 420  
 448 CAATCTTAAAGCGGAATTCATAACGTGATTCGATGTAAGATTTAGGACATCAGAAAAG 507  
 421 AAGATGATGCGTATCAATATAAATATGTCGCGCGCGGATATCTTTATATCTAGATATGA 480  
 508 GAAATATAAATAATGATTAATAAATTTGTAGTGCAGGTTATGATA---TGTAAGGGA 564  
 481 ACAGATGAATCGAACAGAACTCAGCGGTGAGCGGTACCGGTTACCGCTTAGGTTATGAC 540  
 565 AAGATGAATTAAGTGGACTTCAGATTACAGCAGTCTTCCAAACCGCTTAGGTTATGAC 624

QY 541 GGTGTTGTATATATATCCGAGAACGTCCTTCCCAATCTTTTACGAGTGGGAGACGGTG 600  
 DB 625 GGTGTTGTATATATATCCGAGAACGTCCTTCCCAATCTTTTACGAGTGGGAGACGGTG 684  
 QY 601 GAATATTTCTGTTAACTGGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTGACGGC 660  
 DB 685 GAATATTTCTGTTAACTGGCAATATATGACCGATGCCAAACGTCATCGAGCAGGTGACGGC 744  
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 DB 745 GTTGGCATTTGACAAATTTGGTTATATACATTTTATGTTAAACGATGTTGTTGCAACTTCT 804  
 QY 721 TATCGCGCTTAAGGATGTCGACGAAAGGAAAGCATCTGCCCAAAATATACGTTGATTTT 780  
 DB 805 TATCGCGCTTAAGGATGTCGACGAAAGGAAAGCATCTGCCCAAAATATATACGTTGATTTT 864  
 QY 781 GATAACAAAACCATGGAATGGCAAGCTGATTAATAATCAGTATGTCGAAATATAAAGAT 840  
 DB 865 GGTAAACAAAACCATGGAATGGCAAGCTGATTAATAATCAGTATGTCGAAATATAAAGAT 918  
 QY 841 GAACCCAAAACCATGGAATGGCAAGCTGATTAATAATCAGTATGTCGAAATATAAAGAT 900  
 DB 919 GAGAAGCAAAAACCATGGAATGGCAAGCTGATTAATAATCAGTATGTCGAAATATAAAGAT 978  
 QY 901 ACCGCGAGTGGCAAGCTGATTAATAATCAGTATGTCGAAATATAAAGAT 960  
 DB 979 ACCGCGAGTGGCAAGCTGATTAATAATCAGTATGTCGAAATATAAAGAT 1038  
 QY 961 TTTTCCATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 1020  
 DB 1039 TTTTCCATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 1098  
 QY 1021 GAGCTTCCGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 1080  
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 QY 1081 AAAACAGAGACAGCAAAACGAGCAGATACAAACCTGCGCTGCGCTGCGCTGCGCTGCGCT 1140  
 DB 1159 CA-----AAATAGCCCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1191  
 QY 1141 AAAATCTTGGATTTCTTAAATAATTTCCGTTGACGAGCGCATGATGGCCATGCGCGTAAG 1200  
 DB 1192 AAAATCTTGGATTTCTTAAATAATTTCCGTTGACGAGCGCATGATGGCCATGCGCGTAAG 1251  
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 DB 1252 TTTGCCATTTCTCTATGCGGATTTTGGTTCATCCGACAAAATTTCTTGTGCAAGGCGT 1311  
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 QY 1321 GTGCGTCTTTGTTGAGTCTTTTGAATCTGTAATGTAATGTAATGTAATGTAATGTAATG 1380  
 DB 1372 GTGCGTCTTTGTTGAGTCTTTTGAATCTGTAATGTAATGTAATGTAATGTAATGTAATG 1431  
 QY 1381 CCGGCAAGTAAACCAAGCGGAGATTAAGGGGAGATTAAGGGGAGATTAAGGGGAGATTAAGGG 1440  
 DB 1432 CCGGCGCAACCGAAGGCG-----GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1479  
 QY 1441 AACGAG 1500  
 DB 1480 AATGGCGAG 1539  
 QY 1501 TCGAAG 1560  
 DB 1540 GCAGGAG 1581  
 QY 1561 GATGAGCGAG 1620  
 DB 1582 GAAGAGCGGAG 1641

Thu Aug 26 10:18:18 2004

1621 GGCGGTTTCAGCAGCATCTCTGCTCCCTAGAGCCTCTAAAGCAGGACATCGACCTT 1680  
1642 GGCAGTTCAAACGCCATCTCTGCTCCCGAGCCTCTAAAGCAGGATATCGACCTT 1701  
1681 TTCTCTGAAGGTATCCGACGGAACAGGATATCCGCAACCGGAAACGGGCGATTAT 1740  
1702 TTCTCTGAAGGTATCCGACGGAACAGGATATCCGCAACCGGAAACGGGCGATTAT 1761  
1741 ACCGGCACTTGGGAAGCGGTATCCGCAACCGGAAACCGGCAATCCAGCGGATGAA 1800  
1762 ACCGGCACTTGGGAAGCGGTATCCGCAACCGGCAATCCAGCGGATGAA 1821  
1801 AAAGCGCAAAAGCAGATTTACCGTTCGATTCGACAGAAATCGATTCGGAAGCTG 1860  
1822 GAAGCGCAAAAGCAGATTTACCGTTCGATTCGCAAGAAATCGATTCGGAAGCTG 1881  
1861 ACCGAGCAAAAGCGGTAGACCTCTTCCATATGGAAGCGGCAAGATTGATGGCAAC 1920  
1882 ACCGAGCAAAAGCGGTAGACCTCTTCCATATGGAAGCGGCAAGATTGATGGCAAC 1941  
1921 GGTTCACCGCAGACAGCGCGCATCGGAGAGCGGCATCAATCTTTCCGGAAATGTTTCG 1980  
1942 GGTTCACCGCAGACAGCGCGCATCGGAGAGCGGCATCGACCTTTCCGGAGGTTTCG 2001  
1981 ACCGACCCCAAAACATTCAGCTAGTAACTCTTCTGCTAGAGGAGGATTTTACGGCCG 2040  
2002 ACCAAACCGCAGATCTTCAAAGCTAATGATCTCTGCTAGAGGAGGATTTTACGGCCG 2061  
2041 CAGCGCGGGAATTCGGCGGTACTATTTTCAATAATGATGGAAATCTCTTAGTATAACT 2100  
2062 AAGCGCGGGAATTCGGCGGTATTTTCAATAATGATGGAAATCTCTTAGTATAACT 2121  
2101 GAAATATTTGAAATGAAGCTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 2160  
2122 GAAGTACTGAAATGAAGTTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGA 2181  
2161 GTTGAAGTGTGTTGGGCAACAGTTGAAGCTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTG 2220  
2182 GCTGATGCTGTGTTG---AACAGTTTAAAC---TGAAGTTTAAACCCCAATTCGCGGTG 2235  
2221 GTATTCGTTGCAAGCAAGATATGCAAGAGGTGGAAGTTGAAGTTGAAGTTGAAGTTGA 2262  
2236 GTATTCGTTGCAAGCAAGATATGCAAGAGGTGGAAGTTGAAGTTGAAGTTGAAGTTGA 2277

RESULT 3  
US-10-282-122A-29815  
; Sequence 29815, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29815  
LENGTH: 2226  
TYPE: DNA  
ORGANISM: Neisseria meningitidis  
US-10-282-122A-29815  
Query Match 63.8%; Score 1442.6; DB 13; Length 2226;  
Best Local Similarity 80.3%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 349; Indels 102; Gaps 9;  
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Db 1 ATGTGTAACCGAATTTATGGCGGCAATCTCTTTGTTGCCCTTACTTTTACGATCTTTGTATC 60  
QY 61 GCGCGCAATTTGGCGGTACAGCTGTTGCGAATCAACGCGGACCGCCCACTCTGTCA 120  
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Db 109 TACCCCGTCACTTTCAAGTCTAAGGACGTTCCCACTTCGCCCTTCCGGGCTTCGGTA 168  
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Db 169 GAAACACCCCGGTCAACCGGCCCGGTCGGTGGGCAATCGGCTGGAGGCGGAAT 228  
QY 241 ATCGCAACTTTTGATAAAATGGTAATGAAATTCGAATAGTAAGCAGCAGAGGATAT 300  
Db 229 ATTGCTTTTCATCGTGAAGATGCGACGGCAATTCGGGATAGCAAAACAGCAGAGAAAG 288  
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QY 361 AAACTTAAAAGGAAATCAACGAGCGGATCTCTTAATGCAACCAATCTACGTCGGATTTA 420  
Db 349 CAGCTTAAAGATAAATTCATCAACCAATCTCTTAATGTAAGATAGGACATCAGAAAT 408  
QY 421 AAAGATGATCGGTATCAATATAATATGTCGGGCGGATATGTTTATATAGATAGGA 480  
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QY 481 ACAGATGAATCGAAACAGACTCAGCGGTTAAGCGGTTACCCACCGCTTAGGTTATGAC 540  
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QY 1006 GAAGAGCTTGGCGGACGGTTTTATCAGCAACGACAGCGTATTCGGCGTATTCGAGGC 1065  
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QY 1078 A---AAAAACAGACAGCAACGACAGATACAAAACCTTGCCTGCGCTCGAATA 1134  
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QY 1066 AAACAAAAACAGACGCAATCAACGCAATCAGATACAAATCTGCTATGCGGCTCGAATA 1125  
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QY 1126 CACACCAAAATCTCGATCTCTGAAATTTCCGTTGACGAGCGCACTGATGCAATGCC 1185  
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QY 1315 ATGACCGTCCGCTGCTTGTGGAATTTTGGTACCTATGTGAACCTCGGACGATATAAAC 1374  
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QY 1306 ATGACCGTCCGCTGCTTGTGGAATTTTGGTACCTATGTGAACCTCGGACGATATAAAC 1365  
DB |||||  
QY 1375 GATCGCCCGCAAGTAAACCAAGCGCAAGGATGAAATTCGGAAGATGAAATTTGGTGAA 1410  
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QY 1366 GACCGCCCGCAAGTAAACCAAGCGCAAGGATGAAATTCGGAAGATGAAATTTGGTGAA 1425  
DB |||||  
QY 1411 GGGGAGATGAAGGGTGCAGGCTTTGATAACGACGAAAGGAAAGCGAGGCGGTA 1470  
DB |||||  
QY 1426 AGCGAGGAAATGAAGAGGATTTGGTCTGTAAGAAACACGGAAGCGAGTCTGTA 1485  
DB |||||  
QY 1471 GAAGACGAAGCGCGGAGGAGGAACTTCCGAGAGATTAATGCGGAAGACGAGAA 1530  
DB |||||  
QY 1486 GAAGATGAAGACGAGGAGGAGGAACTTCCGAGATGTTAAGTGAAGACGAGAA 1545  
DB |||||  
QY 1531 GCAACCGCGGAGGAGGAACTTGAAGAGGATTTGATGAGCGGCAAGGAGGAGTGAAGAA 1590  
DB |||||  
QY 1546 GAAATCGCGAA-----GAAGATGATGAAGCGGAGGAGGAGGAGTGAAGAA 1596  
DB |||||  
QY 1591 CCGGAGAAATAATCGCGGAGAGGCAAC---GGCGGTTTCAGCGAGCATCTGCGCTGCC 1647  
DB |||||  
QY 1597 CCGGAGAAATAATCGCGGAGAGGCGGCGGTTGCGGTTTCAGCGCATCTCCCGCGCT 1656  
DB |||||  
QY 1648 CTAGAGCTCTTAAGCGGAGGACATCGACCTTTTCTGAAAGGTATCCGACGCGGAA 1707  
DB |||||  
QY 1657 TCGGAAGCCCTTAAGCGGAGGACATCGACCTTTTCTGAAAGGTATCCGACGCGGAA 1716  
DB |||||  
QY 1708 ACGGATATTCGCAAGCGGAGCGGCAATATACCGCACTTTGGGAGCGGCTATCGCG 1767  
DB |||||  
QY 1717 GCCGACATTCGCAAACTGGAAAGCACGCTATACCGCACTTGGGAGCGGCTATCAGC 1776  
DB |||||

QY 1768 AAACCCATTCATGGGACAAATCAGGCGGATGAAAAAGCGGCAAGCAGAAATTTACCGTT 1827  
DB |||||  
QY 1777 AAACCCATTCATGGGATATAAGGCGGATATAAAAAGCGGCAAGCAGAAATTTGACGTT 1836  
DB |||||  
QY 1828 GATTTGCAAGAATAATCGATTTCCGAAAGCTGACGAGCAAAACGCGGTAGAACCTGCT 1887  
DB |||||  
QY 1837 GATTTGCGGAGAAATCGATTTCCGAAACGCTGACGAGAAACGCGGTAGAACCTGCT 1896  
DB |||||  
QY 1888 TTTCAATATTGAACACGCAAGATTGATGCAACGCTTTTCCACGCAAGCGGCTAGAACCTGCT 1947  
DB |||||  
QY 1897 TTTCAATATTGAACAAAGGTGATGATGCAACGCTTTTCCACGCAAGCGGCTAGAACCTGCT 1956  
DB |||||  
QY 1948 GAGAGCGCATCAATCTTTCCGAAATGTTTCCGAAAGCTGACGAGCAAAACGCGGTAGAACCTGCT 2007  
DB |||||  
QY 1957 GATAACCGCATCAATCTTTCCGAAATGTTTCCGAAAGCTGACGAGCAAAACGCGGTAGAACCTGCT 2016  
DB |||||  
QY 2008 AATCTTCGTTGAGAGGAGATTTTACGCGCGGAGCGGCGGAAATGGGCGGTAATTT 2067  
DB |||||  
QY 2017 GATCTTCGTTGAGAGGAGATTTTACGCGCGGAGCGGCGGAAATGGGCGGTAATTT 2076  
DB |||||  
QY 2068 TTTCAATATTGATGGGAAATCTCTAGTATACTGAAATATTTGAAATGAAAGCTGAAGCT 2127  
DB |||||  
QY 2077 TTTCAATATTGATGGGAAATCTCTAGTATACTGAAATATTTGAAATGAAAGCTGAAGCT 2123  
DB |||||  
QY 2128 GAAGTTGAAGTTGAAGCTGAAGCTGAAGTTGAAGTTGAAGCTGAAGTTGAAGCTGAAGTT 2187  
DB |||||  
QY 2124 -----TGAAATTTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCT 2154  
DB |||||  
QY 2188 GAACCTGATGAAGTTTAAACACAAATTCGCGGCTGATTTTCGCGGAGGATATGCAAG 2247  
DB |||||  
QY 2155 GAAC---TGAAATTTAAACCCCAATTCGCGGCTGATTTTGGTTCGAAAGATATGCAAG 2211  
DB |||||  
QY 2248 GAGGTGGAATAATGA 2262  
DB |||||  
QY 2212 GAGGTGGAATAATGA 2226  
DB |||||

## RESULT 4

US-10-735-098-5  
; Sequence 5, Application US/10735098  
; Publication No. US20040131634A1  
; GENERAL INFORMATION:  
; APPLICANT: Pettersson-Fernholm, Annika Margareta  
; APPLICANT: Tomassen, Johannes Petrus Maria  
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein  
; FILE REFERENCE: B45106C1  
; CURRENT APPLICATION NUMBER: US/10/735,098  
; CURRENT FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: 09/485,760  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: PCT/EP98/05117  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: GB 9717423.9  
; PRIOR FILING DATE: 1997-08-15  
; PRIOR APPLICATION NUMBER: GB 9805544.8  
; PRIOR FILING DATE: 1998-02-05  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 2226  
; TYPE: DNA  
; ORGANISM: Neisseria meningitidis strain H44/76  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2223)  
US-10-735-098-5

Query Match 63.8%; Score 1442.2; DB 17; Length 2226;  
Best Local Similarity 80.3%; Pred. No. 0;  
Matches 1828; Conservative 0; Mismatches 383; Indels 66; Gaps 9;

QY 1 ATGTGTAACCGCAATATGCGGCAATGTCTTTGTCCTTACTTTTACGATCTTTGATC 60  
|||||

1	ATGTGTAACCGGAATATATGCGGCAATGTCCTTGTGCGCCCTACTTTTGGGCATCTTGTATT	60	1132	AAACACACCAAAATCTTGGATTTCTAAAAATTTCCGTTGACGAGGCGACTGATGGCCAT	1191
61	GGCGGCAATTTCCGCGTACAGCTGTTGTTCGAATCAACGCGCGACCGCGCCAACTCTGTCA	120	1126	AAACACACCAAAATCTTGGATTTCTGAAATTTTCGTTGACGAGGCGACGGATAAAAAAT	1185
61	GGCGGCAATTTCCGCGTACAGCTGTTGTTCGAATCAACGCGCGACCGCG-----	108	1192	GCCCGTAAGTTTGCATTTCCCTCTATGCCCGATTTTGGTCATCCCGCAAACTCTTGTGTC	1251
121	GATTTCCAAATCTTCCAACTCTGCGGATTAAGCTGCTCCAGTCTGCGGAGCCTTCGGTA	180	1186	GCCCGCGCTTTGCAATTTCCCTCTGCGGATTTTGGCCATCCCGCAAACTCTCTTGTGTC	1245
109	TACCCCGTCACTTTCAAGTCTAAGGACGTTCCCACTCGCCCCCTGCCAAACCTTCTATA	169	1252	GAAGGGGTGAATTTCCCTTTGGTAAACGAAGAAACAAATCATCAAGCTTGCAGCGGAGG	1311
181	GAATACAGCGCGT-----CAAGCGCCCGCTCGGTGCGGCAATGCGGCTCCCAAGG	234	1246	GAAGGGGTGAATTTCCCTTTGGTAAACGAAGAAACAAATCATCAAGCTTGCAGCGGAGG	1305
169	GAACACCAAGCGCGTCAACCGGCGCTCGGTGCGGCAATGCGGCTCTGTGAGG	228	1312	AAATATGACCGTCCGCTGCTTGTGCGACTTTTGTACCTATGTGAAATCTCGAGCGGATATA	1371
235	CGGAATATCGCAACTTTTGTATAAAAAATGGAATGAATTTCCCAATAGTAAGCAGCAGAG	294	1306	AAATATGACCGTCCGCTGCTTGTGCGACTTTTGTACCTATGTGAAATCTCGAGCGGATATA	1365
229	CGGAATTTTCGCAACTTCTGTAAGTTCGCAATGATTTTCCAAATAGCAAAACAGACAA	288	1372	ACCGATCGCCCGGCAAGTAACCAAGCGCGAAGTAAGGGAGGATGAAGAGGTTGCA	1431
295	GAGTATCTGCGCTCAAGAGAGAGATATCTGTTTGTAGACGGTACGCCGAAGAACAG	354	1366	ACTGACCGCCAGCAAGTAAACCAAGCGCGAAGTAAGGGAGGATGAAGAGGTTGCA	1425
289	GAAGAAGCTGTGTTTAAAGAAAGTGTGTTCTGTTTATACGGTTCAAAAAAAGATATA	348	1432	GGCGTTGATTAACGACGAGAAAGC---GAAGACGAAGCCGTAGAGACGAAGGCGGCA	1488
355	GCTGACAAACTTAAAGGAATCAACGAGCGCATCTTAATGACCAATCTACACGTCC	414	1426	GGCGTTGATTAACGACGAGAAAGC---GAAGACGAAGCCGTAGAGACGAAGGCGGCA	1485
349	CTTCAGTGGCTTAAGGATAAAATTCATCAACGCAATCTTAATGTAGAAATTAGGACATCA	408	1489	GAAGACGAAACTTTCGGAAGAGGATTAATCGCGAAGACGAAGAACCCCGCGAAGAA	1548
415	GATTTAAAGATGATGCGTATCAATATAAATATGTCCGCGCGGATATGTTTATATCTAGA	474	1486	GAAGACGAAACTTTCGGAAGAGGATTAATCGCGAAGACGAAGAACCCCGCGAAGAA	1536
409	GAATATGAATAAATAATATGTTATGTAATTTGGTATGCGGTTATGTAATATCTATA	468	1549	ACCGAAGAGTTGATGAAGCCGAGAGAGGAGTTGAAGAACCCCGAAGAAATTCGCGG	1608
475	TATGGAACAGATGAATCGAACAGAACTCAGCGCGGTAGCGGTTACCCACGCTTAGT	534	1537	AACGAAGCGCGCGAAGACGAAGCTGAAGAACCTGAAGAACCCCGAAGAAATTCGCGG	1596
469	AACGGAACAGATGAATTTGAGTGAGCTTCAAAATCGCAAGCAGTTTCTAATCGTTTGGC	528	1609	GCAGAGGCAAC---GGCGTTTCAGCGACGATCTCTGCTGCTGCTAGAGACCTCTAAAGC	1665
535	TATGACGGTTTGTATATTTATTCGAGAACGCTCTTCCCAATCTTTACCGAGTGGGA	594	1597	GCAGAGGCGCGGTGTTGTTTCAACGCGATCTCTGCGCTCCGGAAGCTCTAAAGC	1656
529	TACGACGGTTTGTATATTTATTCGAGAACGCTCTTCCCAATCTTTACCGAGTGGGA	588	1666	AGGACATCGACCTTTTCTGAAAGGATTCGCGACGCGAAGAACCGATTTTCGCAAGC	1725
595	ACGGTGGAAATTTCTGTAAGTGGCAATATATGACCGATGCGCAACGCTCATCGAGCAGT	654	1657	AGGATATCGACCTTTTCTGAAAGGATTCGCGACGCGAAGAACCGATTTTCGCAAGC	1716
589	ACGGTGCATATTCGCGTAACGCAATATATGACCGATGCGCAACGCTCATCGAAACGGA	648	1726	GAACGCGCGCTATTAACGCGCACTTGGGAAGCGCTATCGCAAAACCCATTTCAATGGGAC	1785
655	CAGGC---GGTGGCATGACAAATTTGGTATATACATTTTATGTAACGATTTGTT	711	1717	GGAAAGCACGCTATATACCGGCACTTGGGAAGCGCTATCGCAAAACCCATTTCAATGGGAC	1776
649	AAAGCAGGAGATCCTAGCGAAGATTTGGTATCTCGTTTATTTACGGTCAAAATGTCGA	708	1786	AATCAGCGCGATGAAGAACCGCAAAAGCAGAAATTTACCGTTGATTTTCGCAAGAAATCG	1845
712	GCACCTTCTATCGGCTAAGGATGTCGACGAAAGGAAAGCATCTGCAAAATATACG	771	1777	AATCAGCGCGATGAAGAACCGCAAAAGCAGAAATTTACCGTTGATTTTCGCAAGAAATCG	1836
709	GCACCTTCTATGCTGCGCTGCGGACGACCGGAGGGAACATCTCTGCGGAATATACG	768	1846	ATTTCCGGAAGCTGACGAGCAAAACCGCGTGAACCTGCTTTCCATTTTGAAGACGGC	1905
772	GTTGATTTTGATAACCAAAACCATGAATGGCAAGCTGATTAATAATTCAGTATGCGGAAT	831	1837	ATTTCCGGAAGCTGACGAGCAAAACCGCGTGAACCTGCTTTCCATTTTGAAGACGGC	1896
769	GTTGATTTTGATAAAGAACTTTGAAGGGTCAATTAATTAATAATCAGTATGTCGAAAG	828	1906	AAGATTTGATGCGCAACGCTTCCACGACGACGCGCACTCGGAGAGCGGCATCAATCTT	1965
832	AAAAAGATGAACCAAAACCGCTGACCAATTTACGACATTTACTGCAAAATTTGACGCGC	891	1897	GTGATTTGAGGCGCAATGGTTTCCACGCGACGACGCGCACTCGGAGTAACGCGCATCACTT	1956
829	AAAAACGATGAA---AAGAAACCACTGACCAATTTACGACATTTACCGCAACATTTGACGCGC	885	1966	TCGGAATATGGTTTCGACCGCAACCCCAAAACATTCGAAAGCTAGTAAATCTTCTGTGTAAGGA	2025
892	AACCGCTTTACCGGACGTCAGGTCATCTGATTTAGCGAATACTTTCGCGGTAAT	951	1957	TCGGAATATGGTTTCGACCGCAACCCCAAAACATTCGAAAGCTAGTAAATCTTCTGTGTAAGGA	2016
886	AACCGCTTTACCGGACGTCAGGTCATCTGATTTAGCGAATACTTTCGCGGTAAT	945	2026	GGATTTTACCGCGCGCAGCGCGGGAATTTGGCGGTACTATTTTCAATATGATGGGAAA	2085
952	GAGCGTTTGTATTTTCCATGCGGATGCGGATCAGCGGCTTGAAGCGGTTTTCGCGGAT	1011	2017	GGCTTTTACCGCGCGCAGCGCGGGAATTTGGCGGTACTATTTTCAATATGATGGGAAA	2076
946	GAGCATTTGTTTTCATACCGATACCGATCAGCGGCTTGAAGCGGTTTTCGCGGAT	1005	2086	TCCTTTAGTATTAATGAAATATTTGAAATGAACTGAACTGAACTGAACTGAACTGAACT	2145
1012	AACGGAAGAGCTTTCGCGGACGCTTTATCAGCAACGACACGATTTTCGCGGTATTC	1071	2077	TCCTTTAGTATTAATGAAATATTTGAAATGAACTGAACTGAACTGAACTGAACTGAACT	2112
1006	AAGGGGGAAGCTTTCGCGGACGCTTTATCAGCAACGACACGATTTTCGCGGTATTC	1065	2146	GAAGCTGAAGTTGAAGTTGAAGCTGATTTGGCGCAACAGTTAGAACCTGATGAAGTTAAA	2205
1072	GCAGCAAAAAACAGACAGCAAGCAACGACGACAGATACAAACCTGCGCTCGCGTGA	1131	2113	GAAGCTGAAGTTGAAGTTGAAGCTGATTTGGCGCAACAGTTAGAACCTGATGAAGTTAAA	2169
1066	GCAGCAAAAAACAGACAGCAAGCAACGACGACAGATACAAACCTGCGCTCGCGTGA	1125			

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Qy 2206 CACAAATTGGCGTATTCGGTCCGGAAGAAAGATATGACGAGGTGGAATAATGA 2262
Db 2170 CCCCAATTGGCGTATTCGGTCCGGAAGAAAGATATGAGAGGTGGAATAATGA 2226

RESULT 5
US-10-735-098-9
; Sequence 9, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10735,098
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain 881607
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2121)
US-10-735-098-9

Query Match
Best Local Similarity 57.1%; Score 1291.8; DB 17; Length 2124;
Matches 1676; Conservative 0; Mismatches 417; Indels 54; Gaps 8;

Qy 1 ATGTGTAAACCGAATTATGGCGGCAATCTCTGTGTCCTTACCTTTAGCACTCTGTATC 60
Db 1 ATGTGTAAACCGAATTATGGCGGCAATCTCTGTGTCCTTACCTTTAGCACTCTGTATC 60

Qy 61 GGCGGCAATTTGGCGGTACAGCTGTCTGTAATCAACGCGGCGGCGGCGGCGGCGGCGG 120
Db 61 GGCGGCAATTTGGCGGTACAGCTGTCTGTAATCAACGCGGCGGCGGCGGCGGCGGCGG 120

Qy 121 GATTCCTCAATCTTCCAAATCTGCGGATAGAGCTGCTCCAGCTCTGCGGAGCTTCGGTA 180
Db 109 TACCCCGTCACTTTCAAGTCTTAAGGAGCTTCCCACTTCCGCTCTGCGGCTCTTCGGTA 168

Qy 181 GAAATCACGCGGTCGAAGCGCGCGCGTCTGGTCCGCAATGCGGTCGCCAAGCGGAAT 240
Db 169 GAAACACGCGGTCGAAGCGCGCGCGTCTGGTCCGCAATGCGGTCGCCAAGCGGAAT 228

Qy 241 ATCGCACTTTTGAATAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 300
Db 229 ATTGCACTTCTGATAAGGATGCAATGATTTTCCAAATGAGCAATGAGCAAGCAAGAAAG 288

Qy 301 CTGCGGTCGAAGAGAGGATCTCTGTTTATGAGGATAGAGGATAGAGGATAGAGGATAGAG 360
Db 289 CTGCGGTCGAAGAGAGGATCTCTGTTTATGAGGATAGAGGATAGAGGATAGAGGATAGAG 348

Qy 361 AAATCTTAAAGAGGAAATCAACGAGCGCATCTTAATGCAACCATCTACGTCGGAATTA 420
Db 349 CAGCTTAAAGATAAATTTGTCACCAATCTTACGCGAGCATTAACCATCGGAAGAG 408

Qy 421 AAGATGATCGGATCAATTAATATGTCGCGGCGGATATGTTTATGATGATGATGATGATGAT 480
Db 409 AAAAAATAAATAATGATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 468

Qy 481 ACAGATGAATCGAACAGAACTCAGCGGATAGCGGTTTACCACCGCTTAGGTTATGAC 540
Db 481 ACAGATGAATCGAACAGAACTCAGCGGATAGCGGTTTACCACCGCTTAGGTTATGAC 540
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Db 469 AAAGATGAAATTGAGTGGACTTCAAATTTACAAGCAGTCTACCAACCGTTTGGTTATGAC 528
Qy 541 GGTTCCTGTATATATTCGGGAGAACGCTCTTCCAAATCTTTTACCGAGTGCAGGAAACGGTG 600
Db 529 GGTTCCTGTATATATTCGGGAGAACATCTTTCGCAATCTTTTACCGAGCGGGAACGGTG 588
Qy 601 GAATATTTCTGTAACTGGCAATATATCACCGATGCCAAACGTCATCCAGCAGGTTCAGGC- 659
Db 589 AAATATTTCCGCAACTGGCAATATATGACCGATGCCCAATCTATCGTCAAAATGCGGAGCA 648
Qy 660 --GGTTGGCATTTGACAAATTTGGTTATATCACATTTTATGGTAAACGATTTTGGTGCRACT 717
Db 649 GGAGATCTTACGCAAGATTTGGTTATATCGTTTATTCGTTCAAAATGCGGAGCAACT 708
Qy 718 TCTTATGCGGCTAAGGATGTCGACGAAAGGAAAGCAATCTCTCCAAATATACGTTGAT 777
Db 709 TCTTATGCGGCTAAGGATGTCGACGAAAGGAAAGCAATCTCTCCAAATATATACGTTAAT 768
Qy 778 TTTGATTAACAAACCAATGATGCAAGCTGATTAAATAATCAGTATGTCGAATAAATAA 837
Db 769 TTCGACCAAAACCTGTAATGCAAGCTGATTAAATAATCAGTATGTC---AAAAGAGA 825
Qy 838 GATGAACCCAAACCAACCGCTGACCAATTTACGACATTTACTGCAAAATTTGACGCAACCGC 897
Db 826 GATGATCTTAAACCAACCACTGACCAATTTACGACATTTACTGCAAAATTTGACGCAACCGC 885
Qy 898 TTTACCGGCGAGTCCCAAGCTCAATCTGATTTAGCGAAACCTTTCGCGTATAGCGT 957
Db 886 TTTACCGGCGAGTCCCAAGCTCAATCTGATTTAGCGAAACCTTTCGCGTATAGCGT 945
Qy 958 TTTGTTTTCCATGCGGATGCGGATCAGCGGCTTGGGGCGGTTTTCGCGGATAGGGG 1005
Db 946 TTTGTTTTCCATGCGGATGCGGATCAGCGGCTTGGGGCGGTTTTCGCGGATAGGGG 1077
Qy 1018 GAAGAGTTCGCGGAGCGTTTATCAGCAACGACCAACAGCGTATTCGCGTATTTCCAGCG 1077
Db 1006 GAAGAGTTCGCGGAGCGTTTATCAGCAACGACCAACAGCGTATTCGCGGATAGGGG 1065
Qy 1078 A---AAAAACAGAGACAGCAAAACGACGATCAAAACCTGCGCTCCGCTCTGAAAA 1134
Db 1066 AAACAAAAACAGAGACAGCAAAACGACGATCAGATCAAACTCTGCGCTCCGCTCTGAAAA 1125
Qy 1135 CACACCAAAATCTTGGATTTCTTAAATAATTTCCGTCGAGGCGACTGATGGCGATGCC 1194
Db 1126 CACACCAAAATCTTGGATTTCTTAAATAATTTCCGTCGAGGCGAAGTGGTGAATAATCCC 1185
Qy 1195 GCTAAGTTTGCATTTCTCTATGCGGATTTTGGTTCATCCGACAAACTTCTTGTGCA 1254
Db 1186 CGACCGTTTGGAGTTTCCACTATGCGCGATTTTGGTTCATCCGACAAACTTCTTGTGCA 1245
Qy 1255 GGGCGTGAATTTCTTGGTAAACGAGAAACAAATCAATCAAGTTTCCGACGCGAGAA 1314
Db 1246 GGGCGTGAATTTCTTGGTAAACGAGAAACAAACCAATCAATCTTTCGCGACGCGAGAA 1305
Qy 1315 ATGACCGTCCGCTGTTTGGGACTTTTTCGACCTTCTGAACTGCGAACGATTAATAACC 1374
Db 1306 ATGACCGTCCGCTGTTTGGGACTTTTTCGACCTTCTGAACTGCGAACGATTAATAACC 1365
Qy 1375 GATCGCGCGGCAAGTAAACCAAAGCGGAGATTAAGGGGAGGATCAAGAGGGTGCAGGC 1434
Db 1366 GAAACCGCGCGGCTCCCAACGAGGCGGAGGATGAAGAGGGGACCAAGAGGGTGTAGGC 1425
Qy 1435 GTTGTAAACGACGAGAAAGCGAGACGAGCGGTGAGAGAGAGAGCGGCGCGAGAGAGAC 1494
Db 1426 GTTGTAAACGAGTAAAGAAAGCGAGAAATTCGCGATGAAGAAAGACCCGAGAGAGAA 1485
Qy 1495 GAAACTTCGGAAGAGGATTAATGGCGAAGACGAGAGCAACCGCGGAGAGAAACCGAA 1554
Db 1486 G-----TCGTAGAGATGAAGACGAGATGAAG-----CGAAGAGAAATTCGAA 1530
Qy 1555 GAACTTGTAGAGCGAAGAGAGGAGGAGTTTGAAGAACCCGAGAAATAATTCGCGCGAGAA 1614
Db 1531 GAAAGAACCTGAAGAGAGAGCTGAAGAGGAGAAACCCGAGAGAGAAATTCGCGCGAGAGAA 1590
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Db 1066 CAAAAACAGACAGACAGCAACGATCAGATACAAATCTGCCCTGCGCTCTGGAACAC 1125
Qy 1138 ACCAAATCTTGGATTCTCTAAAAATTTCCGCTTGCAGAGCGGACTGATGCCATGCCCGT 1197
Db 1126 ACCAAATCTTGGATTCTCTAAAAATTTCCGCTTGCAGAGCGGACTGATGCCATGCCCGT 1185
Qy 1198 AAGTTTGCATTTCTCTATGCGCGGATTTTGGTTCATCCGACAAATCTTGTCTGAAGGG 1257
Db 1186 AAGTTTGCATTTCTCTATGCGCGGATTTTGGTTCATCCGACAAATCTTGTCTGAAGGG 1245
Qy 1258 CGTGAATTTCTTTGTTAAAGAGAAACAAATCAAGTTTCCGACGGCAGGAAATG 1317
Db 1246 CGTGAATTTCTTTGTTAGCAAGAGAAACCAATCGAGTTGCCGACGCGAGAAATG 1305
Qy 1318 ACCGTCGCTGCTTCTGCGACTTTTTCACCTATGTGAATTCGACGGATAAACCCGAT 1377
Db 1306 ACCATCGTCTGCTTCTGCGATTTTCTGACCTATGTGAATTCGACGGATAAACCCGAC 1365
Qy 1378 CGCCCGCAAGTAAACCAAGCGGAGATTAAGGGGAGGATGAAGAGGCTGACGGCTT 1437
Db 1366 CGCCCGCGCTCAACCGAAGCGCGAGGATGAAGAGGATTCGACATTTGATATGCGAA 1425
Qy 1438 GATAACGACGAAGAA--CGAGAGAGAGCGGTGAAGACGAAGCGCGGAGAGAC 1494
Db 1426 GAAGCGAAGACGAATTTCCGAGAGATTAACCGCGAAGATGAAGTCAACCGAAGAG 1485
Qy 1495 GAAACT-----TCCGAGAGGATTAATGCGAGACGAGAGCAACCGCGGAGAGAA 1548
Db 1486 GAAGCTGAAGAACCGAAGAGAACTGATGAAGACGAGAGAGAGAAACCGGAGAACT 1545
Qy 1549 ACCGAAGAGTTGATGAAGCCGAAGAGGAGGAGTTGAAGAACCCGAGAGAAATCGCG 1608
Db 1546 GAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAAATCGCG 1605
Qy 1609 ---CGAAGGCAACGGCGTTCCGACGATCTGCTGCTTGAAGCCCTTAAAGC 1665
Db 1606 ACAGAGAGGCAACGGCGTTTCAGCGACATCTCGCCACTCCGGAAGCTTAAAGC 1665
Qy 1666 AGGACATCGACTTTTCTGAAAGGTATCCGACGGCGGAGGCGCATTTCCGCAAT 1725
Db 1666 AGGACATCGACTTTTCTGAAAGGTATCCGACGGCGGAGGCGCATTTCCGCAAT 1725
Qy 1726 GGAAGCGGCTATTACCGGCACTTTGGAAGCGGCTATCGGCAACCCATTCATGGGAC 1785
Db 1726 GGAAGCACGCTATACCGGCACTTTGGAAGCGGCTATCGGCAACCCATTCATGGGAC 1785
Qy 1786 AATCAGGCGGATG-----AAAAAGCGCAAA 1812
Db 1786 GAAAGCTAGATGCACTACGTCATCAAGAGTAGCTATGCGAATCAAGCGCAAA 1845
Qy 1813 GCAGATTTACGTTGATTTTCAGAAAGAAATCGATTTCCGAAAGCTGACGAGCAAA 1872
Db 1846 GCAGATTTGACGTTGATTTTGGTGGAGTTCGCTTTTCAGGTAAGTTGACAGAAATA 1905
Qy 1873 GGCTAGAACCTGCTTTCCATTTGAAGAGCGGCAAGATTTGATGCAACGGTTTCCAGCG 1932
Db 1906 GATACACCCCGCTTTTATATTGAAGAGGCTGTGATTTGATGCAACGGTTTCCAGCT 1965
Qy 1933 ACAGCGGCTACTGGGAGAGCGGATCAATCTTTCCGGAATGTTGACGACCCCAAA 1992
Db 1966 TTGGCGGCTACTGTAAGATGTTGTTGATTTGCTGGCAAGGTTGCACTTAATCCCAA 2025
Qy 1993 ACATTCAGCTAGTAACTTCTGTTAGAGGAGGATTTTACGCGCGGCGGCGGAA 2052
Db 2026 AGTTTAAAGCCAGTATCTTCTGTAAGAGGAGATTTTATGTTGCGCGGCGGCGAG 2085
Qy 2053 TTGGCGGCTACTTTTCAATAATGATGGAAA 2085
Db 2086 TTGGGTGTAATATTATCGACAGTACCGGAAA 2118
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RESULT 7

US-10-343-561-15

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; Sequence 15, Application US/10343561
; Publication No. US20040126389A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Dalemans, Wilfried
; APPLICANT: Denoel, Philippe
; APPLICANT: Feron, Christiane
; APPLICANT: Garcon, Nathalie
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Thierry, Georges
; APPLICANT: Thomard, Joelle
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: Vaccines Comprising Outer Membrane
; FILE REFERENCE: B45260
; CURRENT APPLICATION NUMBER: US/10/343,561
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/EP01/08857
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: EP 00956369.3
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: GB 0103170.7
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-561-15
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Query Match 32.3%; Score 730; DB 17; Length 1000;
Best Local Similarity 84.8%; Pred. No. 5.3e-169;
Matches 882; Conservative 0; Mismatches 115; Indels 43; Gaps 4;

Qy 1222 GATTTGTCTATCCCGACAACTTCTTTCGAAGGCGGTGAATTCCTTTGGTAAACGAA 1281
Db 1 GATTTGTCTATCCGACAACTTCTTTCGAAGGCGGTGAATTCCTTTGGTAAACGAA 60

Qy 1282 GAACAATCATCAAGTTTCCGACGCGAGGAAATGACCGTCCGTCGTTGTTGCGACTTT 1341
Db 61 GAGAAACCATCAAGTTTCCGATGCGAGGGAATGACCGTCCGTCGTTGTTGCGACTTT 120

Qy 1342 TTGACCTATGTAACCTCGGACGATATAAACCGATTCGCCGCAAGTAAACCAAGGCG 1401
Db 121 TTGACCTATGTAACCTCGGACGATATAAACCGCAACCGCGGCAAGTAAACCAAGGCG 180

Qy 1402 GAAGATAAGGGGAGGATGAAGAGGTTGACGCGTTCGATACGAGAGGATTAATGGCGAA 1461
Db 181 GAAGATAAGGGGAGGATGAAGAGGTTGACGCGTTCGATACGAGAGGATTAATGGCGAA 240

Qy 1462 GAAGCCGTAGAACGACGAGGCGGCAAGAGAGCAAACTTCCGAAGAGGATTAATGGCGAA 1521
Db 241 GAAGTTTCCGAAGATGAAGGCGAAGAGCGCGAAGATTCGTAAGAGGATTAATGGCGAA 290

Qy 1522 GACGAAGAGCAACCGCGGAGAGAGAACCCGAGAGGATTAATGAAGCGGAGGAGGAA 1581
Db 291 -----ACCGGAAGAGAGAGCTGAAGAGGAGAGGATTAATGAAGCGGAGGAGGAA 333

Qy 1582 GTTGAAGAAACCGCAAGAAATTCGCGGCAAGAG---GCAACCGCGTTCAGGAGGATC 1638
Db 334 GTTGAAGAAACCGCAAGAAATTCGCGGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 393

Qy 1639 CTGCTGCTTGAAGCGCTTAAAGGAGGAGGATTCGACCTTTCTGTAAGAGGATTCGCG 1698
Db 394 CTGCTGCTTGAAGCGCTTAAAGGAGGAGGAGGATTCGACCTTTCTGTAAGAGGATTCGCG 453

Qy 1699 ACGGCAGAGGAGGATTCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1758
Db 454 ACGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 513
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RESULT 10  
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